

# Figure 1

## Fatty Acid Biosynthesis Pathways

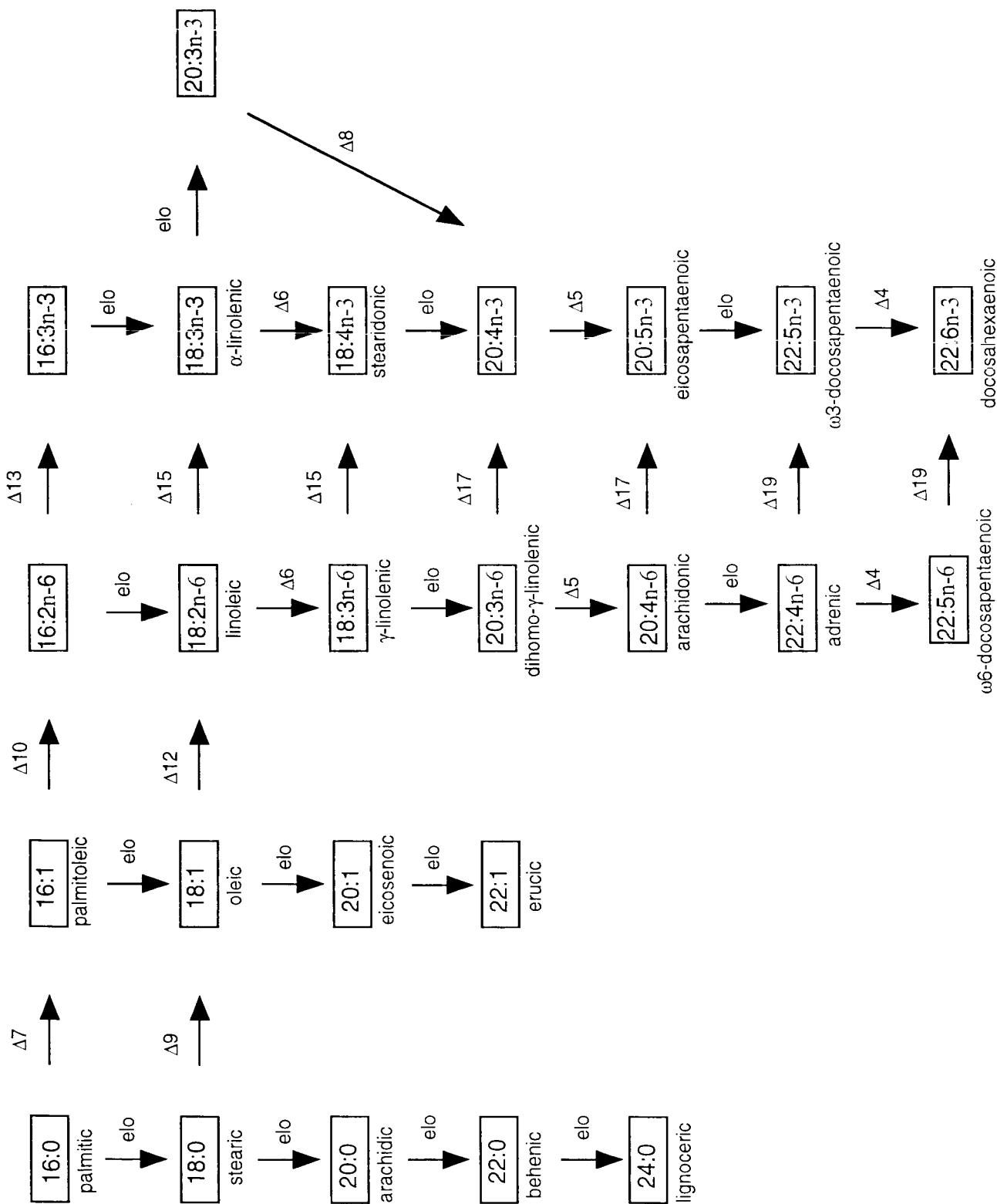


Figure 2

Gap Weight: 6 Average Match: 2.912  
Length Weight: 4 Average Mismatch: -2.003

Quality: 50 Length: 84  
Ratio: 0.625 Gaps: 4  
Percent Similarity: 43.038 Percent Identity: 29.114

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

jojobakcs x ELO2

June 4, 1998 08:23 ..

jojobakcs 24 ATLPNFKSSINLHHVKL.GYHYLISNALFLVFIPLLGLASAHLSFSFSAHD 72  
|.|||.|. :| :| :| :| . | || | ..  
ELO2 66 STLPPVLYAITAYYVIIFGGRFLLSKS..KPF.KLNGLFQLHNLVLTSL 112

jojobakcs 73 LSLFLDLLRRNLLPVVCSFLFVLLATLHFLTRP 106  
|.|| | : |. : : | : : : |.  
ELO2 113 LTLLL.LMVEQLVPIIVQHGLYFAICNIGAWTQP 145

Figure 3

*S. cerevisiae* E102 (AA66-145) with *M. alpina* codon bias

S T L P P V L Y A I T A Y Y V I I F G G R F L  
TCC ACC CTC CCC CCC GTC CTC TAC GCC ATC ACC GCC TAC TAC GTC ATC ATC TTC GGT GGT CGC TTC CTC  
66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88

<-- R0339

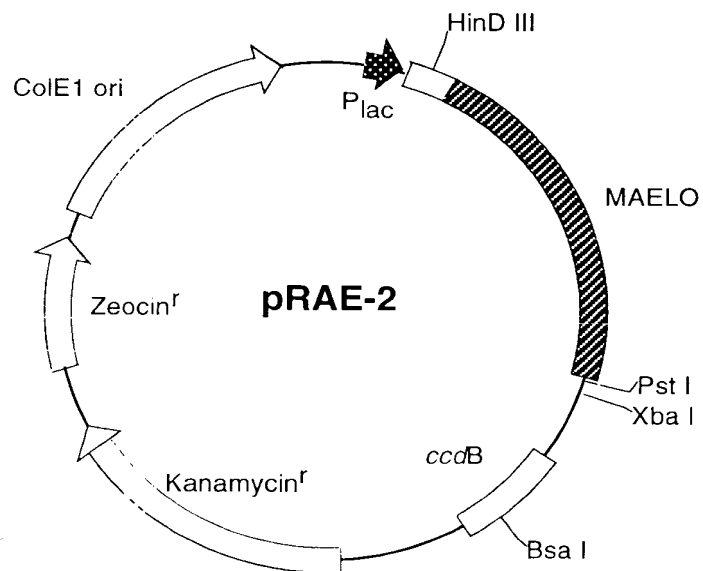
L S K S K P F K L N G L F Q L H N L V L T S L  
CTC TCC AAG TCC AAG CCC TTC AAG CTC AAC GGT CTC TTC CAG CTC CAC AAC CTC GTC CTC ACC TCC CTC  
89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111

S L T L L L L M V E Q L V P I I V Q H G L Y F  
TCC CTC ACC CTC CTC CTC CTC ATG GTC GAG CAG CAG CTC GTC CCC ATC ATC GTC CAG CAC GGT CTC TAC TTC  
112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134

A I C N I G A W T Q P  
GCC ATC TGC AAC ATC GGT GCC TGG ACC CAG CCC  
135 136 137 138 139 140 141 142 143 144 145

**Figure 4**

**A**



**B**

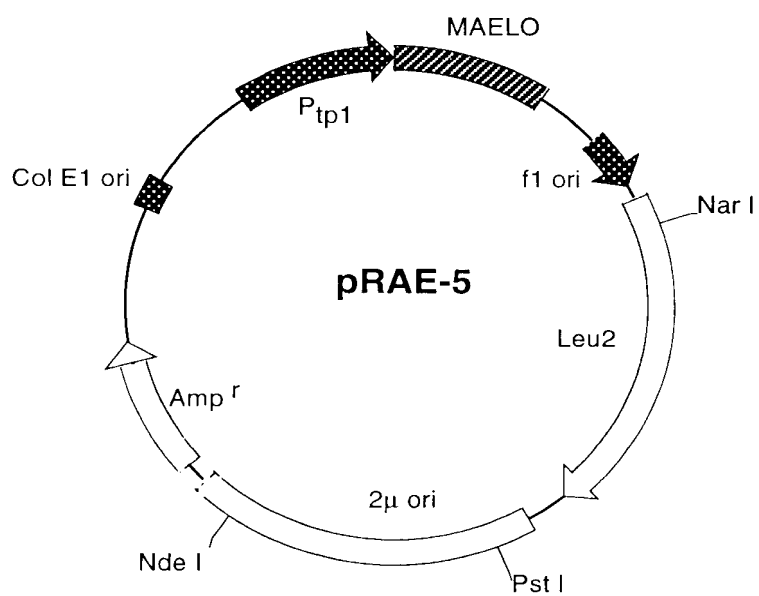


Figure 5

PRAE-5 GAATTCAGG \* \* \* \* \* CATGGCCCGCCCAATCTTGACAA  
PRAE-6 GAATTCAGGCATCTCATGGATCCGCCCATGGCCCGCCCAATCTTGACAA  
EcoRI BamHI NcoI

## Figure 6

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1  ATGGCCGCCG CAATCTTGGA CAAGGTCAAC TTCGGCATTG ATCAGCCCTT
51  CGGAATCAAG CTCGACACCT ACTTTGCTCA GGCCTATGAA CTCGTCACCG
101 GAAAGTCCAT CGACTCCTTC GTCTTCCAGG AGGGCGTCAC GCCTCTCTCG
151 ACCCAGAGAG AGGTCGCCAT GTGGACTATC ACTTACTTCG TCGTCATCTT
201 TGGTGGTTCG CAGATCATGA AGAGCCAGGA CGCCTTCAAG CTCAAGCCCC
251 TCTTCATCCT CCACAACTTC CTCCTGACGA TCGCGTCCGG ATCGCTGTTG
301 CTCTGTTCAT TCGAGAACCT GGTCCCCATC CTCGCCAGAA ACGGACTTTT
351 CTACGCCATC TCGGACGACG GTGCCCTGGAC CCAGCGCCTC GAGCTCCTCT
401 ACTACCTCAA CTACCTGGTC AAGTACTGGG AGTTGGCCGA CACCGTCTTT
451 TTGGTCCTCA AGAAGAAGCC TCTTGAGTTC CTGCACTACT TCCACCACTC
501 GATGACCATG GTTCTCTGCT TTGTCCAGCT TGGAGGATAC ACTTCACTGT
551 CCTGGGTCCC TATTACCCTC AACTTGACTC TCCACGTCTT CATGTACTAC
601 TACTACATGC GCTCCGCTGC CGGTGTTTCG ATCTGGTGGA AGCAGTACTT
651 GACCACTCTC CAGATCGTCC AGTTCGTTCT TGACCTCGGA TTCATCTACT
701 TCTGCGCCTA CACCTACTTC GCCTTCACCT ACTTCCCCTG GGCTCCCAAC
751 GTCGGCAAGT GCGCCGCTAC CGAGGGTGCT GCTCTCTTTG GCTGCGGACT
801 CCTCTCCAGC TATCTCTTGC TCTTTATCAA CTTCTACCGC ATTACCTACA
851 ATGCCAAGGC CAAGGCAGCC AAGGAGCGTG GAAGCAACTT TACCCCCAAG
901 ACTGTCAAGT CCGGCGGATC GCCCAAGAAG CCCTCCAAGA GCAAGCACAT
951 CTAA

```

## Figure 7

1 MAAAILDKVN FGIDQPFGIK LDTYFAQAYE LVTGKSIDSF VFQEGVTPLS  
51 TQREVAMWTI TYFVVIFGGR QIMKSQDAFK LKPLFILHNF LLTIASGSLL  
101 LLFIENLVPI LARNGLFYAT CDDGAWTQRL ELLYYLNYLV KYWELADTVF  
151 LVLKKKPLEF LHYFHHSMTM VLCFVQLGGY TSVSWVPITL NLTVHVFMYY  
201 YYMRSAAQVR IWWKQYLTTL QIVQFVLDLG FTYFCAYTYF AFTYFPWAPN  
251 VGKCAGTEGA ALFGCGLLSS YLLLFINFYR ITYNAKAKAA KERGSNFTPK  
301 TVKSGGSPKK PSKSKHI\*

Figure 8

	1	~ ~ ~ ~ ~	M N S L V T Q Y A A P L F E R Y P Q L H D Y L P T L E R P F F N I S L W E H F D V	50
GNS1	~ ~ ~ ~ ~	~ ~ ~ ~ ~	~ ~ ~ ~ ~	
SUR4	M N T T S T V I A A V A D Q F Q S L N S S S C F L K V H V P S I E N P F . G I E L W P I F S K V			
MAELO	~ ~ ~ ~ ~	~ ~ ~ ~ ~	~ ~ ~ ~ ~	
	51			
GNS1	V T R V T N G R F V P S E F F Q F I A G E L P L S T L P P V L Y A I T A Y Y V I I F G G R F L S K S	100		
SUR4	F E Y F S I . G Y P A E Q I . F E F I H M K T F L A N G Y H A V S I I I V Y Y I I I F G G Q A I L R A L			
MAELO	Y E L V T . G K S I D S . F V F Q E G V T P L S T Q R E V A M W T I T Y F V V I F G G R Q I M K S Q			
	101			
GNS1	K P . F K L N G L F E Q L H N L V L T S L S L L L L M V E Q L V P I I V Q H G L Y F A I C N I G	150		
SUR4	N A S P L K F K L L F E I H N L F L T S I S L V L W L M L E Q L V P M W Y H N G L F W S I C S K E			
MAELO	D A . F K L K P L F I L H N F L L T I A S G S L L L L F I E N L V P I L A R N G L F Y A I C D D G			
	151			
GNS1	A W T Q P L V T L Y Y M N Y I V K F I E F I D T F F L V L K H K K L T F L H T Y H H G A T A L L C Y	200		
SUR4	A F A P K L V T L Y Y L N Y L T K F V E L I D T V F L V L R K K L L F L H T Y H H G A T A L L C Y			
MAELO	A W T Q R L E L L Y Y L N Y L V K Y W E L A D T V F L V L K K K P L E F L H Y F H S M T M V L C F			
	201			
GNS1	T Q L M G T S I S W V P I S L N L G V H V V M Y Y Y F L A A R G I R V W W K E W V T R F Q I I I Q	250		
SUR4	T Q L I G R T S V E W V V I L L N L G V H V I M Y Y Y E L S S I C G I R V W W K Q W V T R F Q I I I Q			
MAELO	V Q L G G Y T S V S W V P I T L N L T V H V F M Y Y Y M R S A A G V R I W W K Q Y L T L L Q I V Q			
	251			
GNS1	F V L D I I G F I Y F A V Y O K A V H L Y F P I L . P H C G G D C V G S T T A T H A G C A I I S S Y L V	300		
SUR4	F L I D L V F V Y F A I Y T F Y A H K Y L D G I L P N K G T C Y G T Q A A A A Y G Y L I L T S Y L L			
MAELO	F V L D L G F I Y F C A Y T Y F A F T Y F P W A . P N V G K C A G T E G A A L F G C G L L S S Y L L			
	301			
GNS1	L F I S F Y I N V Y K R K G T K T S R V V K R A H G G V A A K V N E Y V N V D L K N V P T P S P S P	350		
SUR4	L F I S F Y I Q S Y K K G K K T V K K E S E V S I G . S V A S G S S T G V K I S N T K V S S R K A ~			
MAELO	L F I N F Y R I T Y N A K A K A K A K E R G S N F T P K T V K S G G S P K . K P S K S K H I ~ ~ ~			
	351			
GNS1	K P Q H R R K R			
SUR4	~ ~ ~ ~ ~			
MAELO	~ ~ ~ ~ ~			



# Figure 9

SCORES Initl: 153 Initn: 199 Opt: 495  
57.4% identity in 549 bp overlap

MAELO	150	160	170	180	190	200
	TCTCGAACCAGAGAGAGGTGCGCATGTGGACTATCACTTACTTCGTGTCATCTTTGGTG					
S78624						
	5990	6000	6010	6020	6030	6040
MAELO	210	220	230	240	250	260
	GTGGCCAGATCATGAAGAAGCCAG--GAAGGC-TTCAAGCTCAAGGCCCTCTTCATCCTCC					
S78624						
	6050	6060	6070	6080	6090	6100
MAELO	270	280	290	300	310	320
	ACAACTTCCTCCTGAGGATGCGCTCC--GGATGCTGTGTGCTCCTGTTTCATGAGAACCT					
S78624						
	6110	6120	6130	6140	6150	6160
MAELO	330	340	350	360	370	380
	GGTCCCATCTCTGCGCAGAAAGGACTTTTCTAAGGATCTGCGAGGAGCGGTGCGTGGAC					
S78624						
	6170	6180	6190	6200	6210	6220
MAELO	390	400	410	420	430	440
	CCAGCGCCTGAGAGCTCTCTACTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG					
S78624						
	6230	6240	6250	6260	6270	6280
MAELO	450	460	470	480	490	500
	CAAGCTCTCTTTTGGTCTCAAGAGAGAGGCTCTTGAATTCCTGCACTTCTCCACCACTC					
S78624						
	6290	6300	6310	6320	6330	6340
MAELO	510	520	530	540	550	
	GATGACCATGCTTCTCTGCTTGT---CAAGCTTGGAGGATA-CACTTCAGTGTCTTGG					
S78624						
	6350	6360	6370	6380	6390	6400
MAELO	560	570	580	590	600	610
	GTCCCTATTACCTCAAGTCTGCTCAAGTCTTTCATGTAAGTCTTACATGAGGCTCC					
S78624						
	6410	6420	6430	6440	6450	
MAELO	620	630	640	650	660	670
	GTGGCC---GGTGTGGCATCTGGTGGAGGAGTACTTGAAGCACTCTCCAGATCGTCCAG					
S78624						
	6460	6470	6480	6490	6500	6510
MAELO	680	690	700	710	720	730
	TTGGTCTTGAAGTCTGATTCATCTACTTCTGGGCTTACAGCTACTTGGGCTTCAAGTAC					
S78624						
	6520	6530	6540	6550	6560	6570

Figure 10A

Host(plasmid)	334pCGN7875)	334pYES2)	334pYX242)	334pRAE-5)	334pRAE-6)	334pYX242)	334pRAE-5)
Added substrate	25 $\mu$ M OA	25 $\mu$ M OA	25 $\mu$ M GLA	25 $\mu$ M GLA	25 $\mu$ M GLA	no substrate	no substrate
Fatty acid	lipid ( $\mu$ g)	lipid ( $\mu$ g)	lipid ( $\mu$ g)	lipid ( $\mu$ g)	lipid ( $\mu$ g)	lipid ( $\mu$ g)	lipid ( $\mu$ g)
C16:0	11.948	23.601	35.123	92.011	85.160	16.294	25.34
C16:1	30.665	71.217	32.789	315.464	115.456	56.183	113.913
C18:0	6.185	9.704	10.515	22.628	18.879	5.535	11.092
C18:1n-9	35.340	57.429	33.989	154.386	106.881	28.388	51.538
C18:3n-6			48.856	58.084	12.434		
C20:0			0.474	0.710	0.244		
C20:1n-9	(0.375%)* 0.352	(0.309%)* 0.527		1.405	0.867		0.516
C20:3n-6	ND	ND	(0.092%)* 0.226	(0.324%)* 2.504	(0.269%)* 1.006	ND	ND
C22:0				0.460			
C22:1n-9				0.321			
C24:0					0.315		0.999
Total Lipid	93.760	170.490	245.090	771.690	374.420	112.99	256.52
ND = Not Detected							
% total fatty acid							

Figure 10B

Host(plasmid)	334(pYY242)	334(pYY242)	334(pRAE-5)	334(pRAE-5)	334(pRAE-6)
Added substrate	25 $\mu$ M GLA	25 $\mu$ M GLA	25 $\mu$ M GLA	25 $\mu$ M GLA	25 $\mu$ M GLA
Fatty acid	lipid ( $\mu$ g)	lipid ( $\mu$ g)	lipid ( $\mu$ g)	lipid ( $\mu$ g)	lipid ( $\mu$ g)
C16:0	60.683	61.487	100.998	96.193	66.761
C16:1	79.838	79.586	359.754	220.440	87.359
C18:0	9.784	10.106	15.317	15.165	16.744
C18:1n-9	38.536	39.936	108.472	89.637	71.631
C18:3n-6	17.974	17.833	82.866	56.596	17.766
C20:0			0.510	0.570	
C20:1n-9					
C20:3n-6	(0.136%) * 0.389	(0.130%) * 0.374	(0.336%) * 3.035	(0.401%) * 2.689	(0.353%) * 1.185
C22:0			0.414		
C22:1n-9				0.383	
C24:0			1.513	1.626	
Total Lipid	285.560	288.045	902.560	671.113	335.496
*% total fatty acid					

Figure 12

Host(plasmid)	334(pYX242)	334(pRAE-5)	334(pRELO-1)	334(pRELO-2)
Added substrate	25 $\mu$ M GLA 25°C/48hrs	25 $\mu$ M GLA 25°C/48hrs	25 $\mu$ M GLA 25°C/48hrs	25 $\mu$ M GLA 25°C/48hrs
Fatty acid	Lipid ( $\mu$ g)	Lipid ( $\mu$ g)	Lipid ( $\mu$ g)	Lipid ( $\mu$ g)
C16:0	28.7	76.707	84.424	77.445
C16:1	0.729	2.513	1.532	1.056
C18:0	7.432	15.761	27.17	21.32
C18:1n-9	28.9	77.323	109.419	82.844
<b>C18:3n-6</b>	9.729	29.236	19.085	<b>18.804</b>
C20:0		0.643	0.522	0.537
C20:1n-9		0.77	0.426	0.299
<b>C20:3n-6</b>	<b>(0.185%) * 0.374</b>	<b>(0.279%) * 1.472</b>	<b>(0.153%) * 0.748</b>	<b>(0.200%) * 0.832</b>
C22:0		0.451		
C22:1n-9			0.224	
C24:0		0.918		
Total Lipid	202	527	490	416
*%total fatty acid				

Figure 11

Host(plasmid)	334(pRAE-5/pCCGR4)	334(pYXX242/pYES2)	Host(plasmid)	334(pRAE-5/pCCGR4)	334(pYXX242/pYES2)
Added substrate	25 $\mu$ M GLA	25 $\mu$ M GLA	Added substrate	25 $\mu$ M GLA	25 $\mu$ M GLA
Fatty Acid	lipid ( $\mu$ g)	lipid ( $\mu$ g)		lipid ( $\mu$ g)	lipid ( $\mu$ g)
C16:0	41.050	37.169	C16:0	96.986	32.221
C16:1	99.393	100.552	C16:1n-7	209.667	62.757
C18:0	34.432	27.852	C18:0	80.418	14.027
C18:1	110.631	92.786	C18:1n-9	207.104	28.701
<b>C18:3n-6</b>	<b>15.004</b>	<b>7.924</b>	<b>C18:3n-6</b>	<b>25.264</b>	<b>10.543</b>
C20:0	0.643	0.574	C20:0	2.038	
C20:1	1.996	1.684	C20:1n-9	3.591	
<b>C20:3n-6</b>	<b>0.542</b>	<b>0.607</b>	<b>C20:3n-6</b>	<b>1.284</b>	<b>0.326</b>
<b>C20:4n-6</b>	<b>0.579</b>		<b>C20:4n-6</b>	<b>1.392</b>	
C22:0	1.242	2.604	C22:0	1.124	
C24:0	4.754	4.563	C24:0	3.952	
Total Lipid	334	300	Total Lipid	756	197

# Figure 13

SCORES Init1: 156 Initn: 215 Opt: 296  
 Smith-Waterman score: 296; 28.8% identity in 264 aa overlap

	10	20	30	40	50	60
U61954	RTFKMMDQILGTNFTYEGAKEVARGLEGFSAKLAVGYIATIFGLKYYMKDRKAFDLSTPL					
MAELO	AQAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLK-PL					
	30	40	50	60	70	80
	70	80	90	100	110	119
U61954	NIWNGILSTFSLLGFLFTF-PTLLSVIRKDGFSHTYSHVSELYTDSTSGYWI-----F					
MAELO	FILHNFLLLTIASGSLLLLFIEENLVPILARNGL-----FYAICDDGAWTQRLELLYY					
	90	100	110	120	130	
	130	140	150	160	170	
U61954	LWVISKIPELLDTVFIVLRKRPLIFMHWHYHHALTGYYALVCYHE--DAVHVMVWV-VWMNY					
MAELO	LNYLVKYWELADTVFLVLKKKPLEFLHYFHHSMT---MVLCFVQLGGYTSVSWVPITLNL					
	140	150	160	170	180	190
	180	190	200	210	220	230
U61954	IIHAFMYGYLLKSLKVPIPPSVAQAITSQMVFQFA-----VAIFAQVHVSYKHYVEGVE					
MAELO	TVHVFMYYYYMRSAAGVRI--WWKQYLTLQIVQFVLDLGFIFYFCAYTYFAFTYFPWAPN					
	200	210	220	230	240	250
	240	250	260	270	280	
U61954	-GLAYSFRGTAI-GFFMLTTYFYLWIQFYKEHYLKNGGKKYNLAKDQAKTQTKKAN					
MAELO	VGKCAGTEGAALFGCGLLSSYLLLFIFYRITY----NAKAKAAKERGSNFTPKTVKSGG					
	260	270	280	290	300	
MAELO	SPKKPSKSKHIX					
	310					

# Figure 14

SCORES Init1: 178 Initn: 178 Opt: 318  
 Smith-Waterman score: 318; 33.0% identity in 188 aa overlap

	50	60	70	80	90	100
Z68749	SLLTNQDEVFPHIRARRFIQEHFGLFVQMAIAYVILVFSIKRFMRDREPFQLTTALRLWN					
				:  :: : :: : :: : :: :	:	
MAELO	ELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHN					
	30	40	50	60	70	80

	110	120	130	140	150	160
Z68749	FFLSVFSIYGSWTMFPF--MVQQIRLYGLYGCGCEALSNLPSQAEYWLFLTILSKAVEFV					
	: :	:: : :  :	:   :	: : :	: :	::
MAELO	FLLTIAS--GSLLLLFIEHLVPILARNGLFYAICDD-GAWTQRLELLYLYNLVVKYWELA					
	90	100	110	120	130	140

	170	180	190	200	210	220
Z68749	DTFFLVLRKKPLIFLHWYHHMATFVFFCSNYPTPSSQSRVGVIVNLFVHAFMYPYFTRS					
	:	:	:   :	:       : :	:	: :
MAELO	DTVFLVLKKKPLEFLHYFHHSMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYMRS					
	150	160	170	180	190	200

	230	240	250	260	270
Z68749	MNIKVPAKISMAVTVLQLTQF--MCFIYGCTLMYYSLATNQARYPSNTPATLQCLSYTL				
	: : : :	: :   :   :	:         :	:   : : :	
MAELO	AGVRIWWK--QYLTTLQIVQFVLDLGFYFCAITYFAFTYFPWAPNVGKCAGTEGAALFG				
	210	220	230	240	250

	280
Z68749	HLL

MAELO	CGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHIX				
	270	280	290	300	310

# Figure 15

SCORES Init1: 30 Initn: 30 Opt: 40  
 Smith-Waterman score: 49; 22.1% identity in 86 aa overlap

		10	20	30	40	
AF003134		MLYSITRRCYTFFVTSLSHFYQLYVTECLENVIFNVLVNGQSINSRWKD				
		: : :  :  : : :: :  :  : : :: :				
MAELO		MAAAILDKNVNFQIDQPFQIKLDTYFAQA---YELVTGKSIDSFVFQEGVT--PLSTQREV				
		10	20	30	40	50

	50	60	70	80	90	100
AF003134	AEKTITSFPPHF-----PQTFQOPHILTLHFLFFVSVTLVTVFKKPKCEFPHSLA					
	: : :    : :: ::  :  : :					
MAELO	AMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHNFLLTIASGSLLLLFIENLVPIARNG					
	60	70	80	90	100	110



# Figure 16

## Mouse

SCORES Initl: 161 Inaln: 191 Opt: 325  
Smith-Waterman score: 325; 28.8% identity in 285 aa overlap

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      10      20      30      39      40
U97107  MLTSMNFSRGLKMD--LMQPYDFETFDLRPFLEEWVSSF-----LIVV
      : : : : : | : : : | : : : | : : : | : : : : :
MAELO   MAAAILDKVNFGLDQPFQIKLLTYFAQAYELVTGKSIDSEVFQEGVTPLSTQREVAMWTI
      10      20      30      40      50      60

      50      60      70      80      90      100
U97107  VYLLLIWVGQTYMFTREFSFLQRPILILWSFFLAIFSIILGTLRMWKFMTATVMFTVGLKQTV
      : : : : | : : : : : : : : : : : : : : : : : : : : :
MAELO   TTFVVIKGGHQMFSQDAFTLPLFLFILHIFLLTIAS--GSL-LLLFIENLV-PILARNGL
      70      80      90      100      110

      110      120      130      140      150
U97107  CFAIYTEDAVVRFWSFLFLSKVV---ELGDTAFIILKRPILIFVHWYHHST--VLLFTS
      : : : | : : : : : : : : : : : : : : : : : : : : :
MAELO   FYAICDDGAWTQRLLELLYYLNYLVKFWELADTVFLVLKPKPLEFLHYFHHMTMVLCPVQ
      120      130      140      150      160      170

      180      190      200      210      220      230
U97107  FGYKTHVPSGGEWF-MNNFVGVHSMVITYTMMKAAFLKHPNLLPMVITSIQILQMVLG---
      : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
MAELO   LGGYTSV---SWVFITINLTVHVMTITYYMRSAAGVR--IWWKQFLTLQIVQFVLDLGF
      180      190      200      210      220      230

      240      250      260      270      280      290
U97107  -----TIFGILNYIWPQEHG-CHCTTEHFFWSHMLYGYFILFAHFFHPAYLRPEKIVA
      | : : : | : : : | : : : | : : : | : : : | : : : | : : :
MAELO   TYFCAYTYFAITYFPWAPNVGHCAGTEGAALFGCGLLSSYLLLFINEYRITY-NAKAFAA
      240      250      260      270      280      290

      300      310
U97107  SKSQX
      : :
MAELO   KERGSEFTPTVFSGGSPHPPSPSHIX
      300      310

```

## Human

SCORES Initl: 147 Inaln: 147 Opt: 211  
Smith-Waterman score: 211; 23.7% identity in 150 aa overlap

```

      110      120      130      140      150      160
MAELO   NLVPILARNGLFYAICDDGAWTQRLLELLYYLNYLVKFWELADTVFLVLKPKPLEFLHYFH
      : : : : : : : : : : : : : : : : : : : : :
AC004050 SLIIVVLDLTYILPLCLPGDTIFILFQKLIPLHWYH
      10      20      30

      170      180      190      200      210      220
MAELO   HSMTHVLCPVQLGGYTSVSWVFITINLTVHVMTITYYMRSAAGVR-IWWK--QYLTTLQIV
      | : : : : : : : : : : : : : : : | : : : | : : : | : : :
AC004050 HITVLLYSWYSYKMMVAGSGWENTINYGVAHMTSYIALRAAGFRVSRFFAMEITLSQIT
      40      50      60      70      80      90

      230      240      250      260      270      280
MAELO   QFVLDLGFIFYFCAYTYFAITYFPWAPNVGHCAGTEGAALFGCGLLSSYLLLFINEYRITY
      : : : : | : : : : | : : : : | : : : : | : : : : | : : : :
AC004050 QILMG-----CVVNYLVFC---WMQH-DQCHSHFQNIWSSLMYLSYLVLFCHFFFEAY
      100      110      120      130      140

```

# Figure 17

SCORES Init1: 87 Initn: 218 Opt: 232  
 Smith-Waterman score: 272; 29.7% identity in 232 aa overlap

	40	50	60	70	80	90
MAELO	SFVVFQEGVTPPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILHNFLLTIASGS					
				:   :     :   :   :		
I05465	PRYKSQRMVPPGQLHPYVCLFCYLLTHCMAGTKIHEEPAAVLLPSILQLYNLGLTLLS--					
	20	30	40	50	60	70
	100	110	120	130	140	150
MAELO	LLLLFIENLVPI LARNGLFYAICDDGAWTQRLLELLYYL--NYLVKYWELADTVFLVLKKK					
	:     : : :   :   : : :     :     :   :   :					
I05465	-LYMFYELVTGVWEGKYNFFCQGTRSAGESDMKILRVLWWYYFSKLIEFMDTFFFILRKN					
	80	90	100	110	120	
	160	170	180	190	200	210
MAELO	--PLEFLHYFHH-SMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY-MRSAAGVR--					
	:     :     :   :     :   :     :     :   :					
I05465	NHQITVLHVYHHATMLNIWWFVMNWVPCGHSYFGATLNSFIHVLMSYYGLSSIPSMRPY					
	130	140	150	160	170	180
	220	230	240	250	260	270
MAELO	IWWKQYLTTLQIVQFVLDLGFYFCAITYFAFTYFPWAPNVGKCAGTEGAALFGCGLLSS					
	:       :     :       : :   : : :   :   :   :					
I05465	LWWKKYITQGQLVQFVLTIIQTTCG-----VFWP-----CSFPLGWLFFQIGYMIS					
	190	200	210	220	230	
	280	290	300	310		
MAELO	YLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHIX					
	:               : : : :					
I05465	LIALFTNFYIQTYNKKGASRRKEHLKGHQNGSVAAVNGHTNSFPSLENSVKPRKQRKDXQ					
	240	250	260	270	280	290

## Figure 18

1 MGTDQGKTFT WEELAAHNTK DDLLEAIRGR VYDVTKFLSR HPGGVDTLLL  
51 GAGRDVTPVF EMYHAFGAAD AIMKKYYVGT LVSNELPIFP EPTVFHKTIK  
101 TRVEGYFTDR NIDPKNRPEI WGRYALIFGS LIASYQAQLF VPFVVERTWL  
151 QVVFAIIMGF ACAQVGINPI HDASHFSVTH NPTVWKILGA THDFFNGASY  
201 LVWMYQHMLG HHPYTNIAGA DPDVSTSEPD VRRIKPNQKW FVNHNQHMF  
251 VPFLYGLLAF KVRIQDINIL YFVKTNDAIR VNPISTWHTV MFWGGKAFFV  
301 WYRLIVPLQY LPLGKVLLLF TVADMVSSYW LALTFQANHV VEEVQWPLPD  
351 ENGIIQKDW A MQVETTQDY AHDShLWTSI TGSLNYQAVH HLFPNVSQHH  
401 YPDILAIKN TCSEYKVPYL VKDTFWQAFA SHLEHLRVLG LRPKEE\*

Figure 19

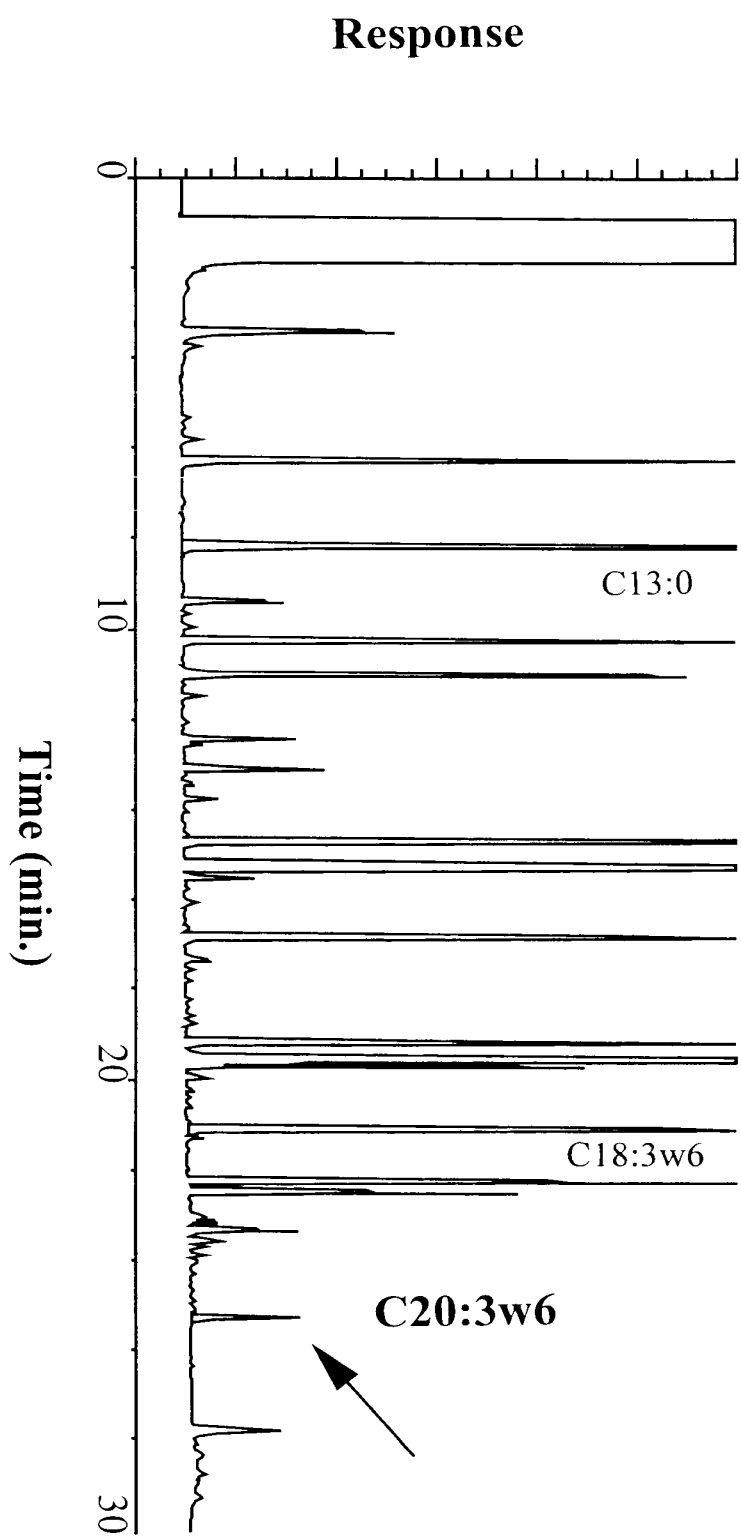
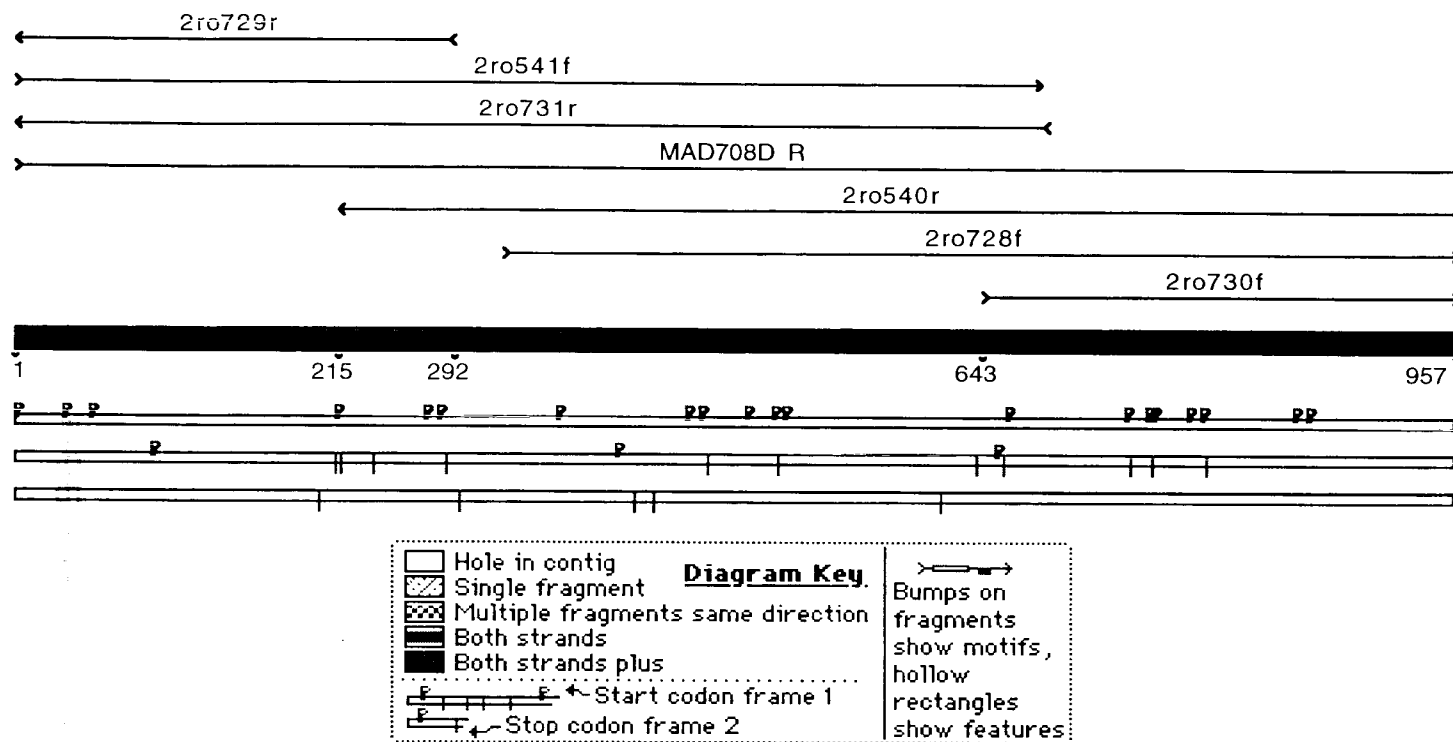


Figure 20

Host(plasmid)	334(MAD708-2)	334 (MAD708-10)	334(MAD708-18)	334 (MAD708-19)	334(MAD708-30)	334 (pRAE5)
Added substrate	25μM GLA	25μM GLA	25μM GLA	25μM GLA	25μM GLA	25μM GLA
Fatty Acid	% total lipid					
C16:0	14.1	14.68	14.38	15.45	14.13	13.59
C16:1	42.84	43.42	42.57	38.03	43.58	43.98
C18:0	3.19	3.28	3.63	4.08	3.37	2.04
C18:1n-9	17.66	19.39	19.6	20.8	20.06	10.88
C18:3n-6	6.65	5.58	10.24	9.46	3.56	11.14
C20:0	0.26	0.3	0.32	0.4	0.46	0.57
C20:3n-6	(47.5%) 6.03	(41.2%) 3.92	(8.0%) 0.91	(21.5%) 2.59	(49%) 3.43	(3.4%) 0.24
Total Lipid (μg)	238.47	307.86	188.51	167.31	207.47	466.65

(% conversion) = product/(substrate+product)

### Figure 21



**Figure 22**

1	ATGGAGTCGA	TTGCGCCATT	CCTCCCATCA	AAGATGCCGC	AAGATCTGTT
51	TATGGACCTT	GCCACCGCTA	TCGGTGTCCG	GGCCGCGCCC	TATGTCGATC
101	CTCTCGAGGC	CGCGCTGGTG	GCCCAGGCCG	AGAAGTACAT	CCCCACGATT
151	GTCCATCACA	CGCGTGGGTT	CCTGGTCGCG	GTGGAGTCGC	CTTTGGCCCCG
201	TGAGCTGCCG	TTGATGAACC	CGTTCCACGT	GCTGTTGATC	GTGCTCGCTT
251	ATTTGGTCAC	GGTCTTTGTG	GGCATGCAGA	TCATGAAGAA	CTTTGAGCGG
301	TTCGAGGTCA	AGACGTTTTT	GCTCCTGCAC	AACTTTGTGTC	TGGTCTCGAT
351	CAGCGCCTAC	ATGTGCGGTG	GGATCCTGTA	CGAGGCTTAT	CAGGCCAACT
401	ATGGACTGTT	TGAGAACGCT	GCTGATCATA	CCTTCAAGGG	TCTTCCTATG
451	GCCAAGATGA	TCTGGCTCTT	CTACTTCTCC	AAGATCATGG	AGTTTGTCTGA
501	CACCATGATC	ATGGTCCTCA	AGAAGAACAA	CCGCCAGATC	TCCTTCTTGC
551	ACGTTTACCA	CCACAGCTCC	ATCTTCACCA	TCTGGTGGTT	GGTCACCTTT
601	GTTGCACCCA	ACGGTGAAGC	CTACTTCTCT	GCTGCGTTGA	ACTCGTTCAT
651	CCATGTGATC	ATGTACGGCT	ACTACTTCTT	GTCGGCCTTG	GGCTTCAAGC
701	AGGTGTCGTT	CATCAAGTTC	TACATCACGC	GCTCGCAGAT	GACACAGTTC
751	TGCATGATGT	CGGTCCAGTC	TTCTTGGGAC	ATGTACGCCA	TGAAGGTCCT
801	TGGCCGCCCC	GGATACCCCT	TCTTCATCAC	GGCTCTGCTT	TGGTTCTACA
851	TGTGGACCAT	GCTCGGTCTC	TTCTACAAC	TTTACAGAAA	GAACGCCAAG
901	TTGGCCAAGC	AGGCCAAGGC	CGACGCTGCC	AAGGAGAAGG	CAAGGAAGTT
951	GCAGTAA				

## Figure 23

1 MESIAPFLPS KMPQDLFMDL ATAIGVRAAP YVDPLEAALV AQAKEYIPTI  
51 VHHTRGFLVA VESPLARELP LMNPFHVLLI VLAYLVTVFV GMQIMKNFER  
101 FEVKTFSSLH NFCLVSISAY MCGGILYEAY QANYGLFENA ADHTFKGLPM  
151 AKMIWLFYFS KIMEFVDTMI MVLKKNNRQI SFLHVVHHSS IFTIWWLVTF  
201 VAPNGEAYFS AALNSFIHVI MYGYYFLSAL GFKQVSFIKF YITRSQMTQF  
251 CMMSVQSSWD MYAMKVLGRP GYPFFITALL WFYMWTMLGL FYNFYRKNK  
301 LAKQAKADAA KEKARKLQ\*



# Figure 24

Host(plasmid)	334(pRPB2)	334 (pYES2)
Added substrate	25µM GLA	25µM GLA
	(n=4)	
Fatty Acid	% total lipid	
C16:0	15.65	15.23
C16:1	35.2	38.59
C18:0	5.68	5.55
C18:1n-9	25.55	25.27
C18:3n-6	3.1	6.75
C20:0	0.36	0.14
C20:3n-6	(62.0%) 5.06	(2.6%) 0.18
Total Lipid (µg)	314	247

(% conversion) = product/(substrate+product)

# Figure 25

**A.**

Host(plasmid)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)
Added substrate	25μM SA	25μM OA	25μM LA	25μM DGLA	25μM AA	25μM Adenic
	C18:0	C18:1n-9	C18:2n-6	C20:3n-6	C20:4n-6	C22:4n-6
Fatty Acid	% total lipid					
C16:0	15.07	14.52	15.74	15.69	16.06	15.15
C16:1	33.7	32.37	32.23	25.65	33.65	33.39
C18:0	*9.78	5.83	5.61	8.33	4.52	5.35
C18:1n-9	31.2	*37.25	26.05	20.15	24.54	28.54
C18:2n-6			*10.4			
C18:3n-6						
C20:2n-6			0.29			
C20:3n-6				*16.5		
C20:4n-6				0.27	*11.7	
C22:4n-6						*7.46
Total Lipid (μg)	132	130	171	55	225	163

**B.**

Host(plasmid)	334(pRPB2)	334(pRPB2)	334(pRPB2)
Added substrate	25μM ALA	25μM STA	25μM EPA
	C18:3n-3	C18:4n-3	C20:5n-3
Fatty Acid	% total lipid		
C16:0	17.32	16.01	20.67
C16:1	27.68	34.31	50.7
C18:0	6.75	5.39	6.14
C18:1n-9	28.4	28.54	
C18:3n-3	*8.39		
C18:4n-3		*1.95	
C20:4n-3		(73.2%) 5.33	
C20:5n-3			*10.33
C22:5n-3			0.25
Total Lipid (μg)	114	199	201

\*indicates substrate added  
(% conversion) = product/(substrate+product)

**Figure 26**

**A.**

Host(plasmid)	334(pRPB2+PRPE31)	334(pYES2+pYX242)
Added substrate	25μM GLA	25μM GLA
Fatty Acid	% total lipid	
C16:0	15.54	18.26
C16:1	30.16	33.51
C18:0	8.76	5.58
C18:1n-9	27	27.37
C18:3n-6	*2.6	*5.6
C20:0	0.4	0.32
C20:3n-6	(57.4%) 3.55	(2.9%) 0.17
C20:4n-6	(27.6%) 1.32	ND
Total Lipid (μg)	254	258

**B.**

Host(plasmid)	334(pRPB2+PRPE31)	334(pYES2+pYX242)
Added substrate	25μM STA	25μM STA
Fatty Acid	% total lipid	
C16:0	18	16.4
C16:1	28.37	34.78
C18:0	7.42	5.71
C18:1n-9	26.44	30.15
C18:4n-3	*2.93	*4.57
C20:0	0.25	0.17
C20:4n-3	4.13	0.32
C20:5n-3	(39%) 1.87	(2.1%) .10
Total Lipid (μg)	257	304

\* indicates substrate added  
(% conversion) = product/(substrate+product)

# Figure 27

SCORES Initl: 114 Initn: 278 Opt: 278  
 Smith-Waterman score: 308; 30.9% identity in 259 aa overlap

	40	50	60	70	80	90	99
GLELO	VAQAEKYIPTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLVTVFVGMQIMKNFE						
	: :  : :: : ::       : :						
MAELO	GIKLDTYFAQAYELVTGKSIDSFVFQEGVTPPLSTQREVAMWTITYFVVIFGGRQIMKSQD						
	20	30	40	50	60	70	
	100	110	120	130	140	150	
GLELO	RFEVKTFSLHNFCLVSI SAYMCGGILYE--AYQANYGLFENAADHTFKGLPMAMKIWL						
	::  : :      :   : : : : :         : : :						
MAELO	AFKLLKPLFILHNFLLTIASGSLLLFIENLVPILARNGLFYAICDDGAWTQRLLELLYYLN						
	80	90	100	110	120	130	
	160	170	180	190	200	210	
GLELO	YFSKIMEFVDTMIMVLKKNRQISFLHVVHSSIFTIWWLVTFVAPNGEAYFSAALNSFI						
	:     : :  :      : :     : : :  : : : : : : :  :  :						
MAELO	YLVKYWELADTVFLVLKK--KPLEFLHYFHHS--MTMVLCFVQLGGYTSVSWVPITLNLTV						
	140	150	160	170	180	190	
	220	230	240	250		260	
GLELO	HVIMYGYFSLGFKQVSFIKFYITRSQMTQF-----CMMSVQS----SWDMYAM						
	:    :    : :   :    :     : : :   : : :   :						
MAELO	HVFMYYYMRSAAGVRI--WWKQYLTTLQIVQFVLDLGFIFYCAITYFAFTYFPWAPNVG						
	200	210	220	230	240	250	
	270	280	290	300	310		
GLELO	KVLGRPGYPFFITALLWFYMWTLGLFYNFYRKNALAKQAKADAAKEKARKLQ						
	:  :     :        : : :       :  :						
MAELO	KCAGTEGAALFGCGLLSSYLL----LFINFYR----ITYNAKAKAAKERGSNFTPKTVKS						
	260	270	280	290	300		
MAELO	GGSPKKPSKSKHIX						
	310						

Figure 28

MAELO	1	-MESIAPFLPSKMPQDLFMDLATAIGVRAAPYVDPLEAALVAQ	42
GNS1	1	-----MNSLVTQYAAPLFEERYPQLHDYLPPTLERPFNISLW	20
SUR4	1	MNTTSTSTVIAAVADQFQSLNSSSSCFLLKVHVPSIENP-FGIEL	36
MAELO	43	AEKYIPTIVHHTRGFLVAVESPLARELPMLNPFHVLLIVLAYL	85
GNS1	21	LDITYFAOAYELVTGKSIDSEFVFOEGVTPLSTQREVAMWTITYF	63
SUR4	37	EHFDDDVAVRTNGRFVPSSEFOFIAGELPLSTLPVLYAITAXY	79
MAELO	43	WPIFSKVFEYFSG-YPAEQFEFIHNKTFLANGYHAVSIIVYX	84
GNS1	86	VTVFVGMOMKKNFERFEVKTFSLLHNFCLVSISAYMCGGILYE	128
SUR4	64	VVIFGGROIMKSODA--FKLKLFIHNFLLTIASSGLLLFI	104
MAELO	80	VIIIFGGRLIS--KSKPFKLNGLFQLHNLVLTSLTLLLMV	120
GNS1	85	IIIFGGQAILRALNASPLKFKLLFEIHNLFLLTSLISLVLLML	127
MAELO	129	--AYO--ANYGLFENAADHTFKGLPMAKMIMLFFYFSKIMEFVD	167
GNS1	105	ENLVPILARNGLFYAICDDGAWTORLELLYLYLVKYMELAD	147
SUR4	121	EOLVPIIVQHGLFYAICNIGAWTORLVTLLYYMNYIVKFIEFID	163
MAELO	128	EOLVPMVYHNGLFWSCSKAEAFAPKLVTLLYLYLVTKFVELID	170
GNS1	168	TMIMVLKKNNRQISFLHVVYHSSIFTIMWLVTTFVAPNGEAYFS	210
SUR4	148	TVFVLVLKK--KPLEFLHYFHHSMTMVLCF-VOLGGYTSVSWVP	187
MAELO	164	TFFLVLKH--KKLTFLHTYHHGATALLCY-TOLMGTPSISWVP	203
GNS1	171	TVFVLVLR--KKLLFLHTYHHGATALLCY-TQLIGRTSVEWV	210
MAELO	211	AALNSFTHVIMYGYFFLSALGFKQVSFIKFIITRSOMTOFCMM	253
GNS1	188	ITLNLTVHVFMYYYYMRSAAAGVR--IWWKQYLTTLQIVOFVLD	228
SUR4	204	ISLNLGVHVVMYYFFLAARGIR--VWWKKEWVTRFOIIOFVLD	244
MAELO	211	ILLNLGVHVIMYYFFLSSCGIR--VWWKQWVTRFOIIOFVID	251
GNS1	254	SVOSSWDMYAMKVLGRPGYPFITALLWFYMWMTMLGLFYNFYR	296
SUR4	229	LGFIYFCAYTYFAFTYFPW-APNVGKCCAGTEGAALFGGLISS	270
MAELO	245	IGFIYFAVYOKAVHLYFP-ILPHCGDCVGSTTATFAGCAIISS	286
GNS1	252	LVFVYFATYTFYAHKKYLDGILPNKGTCTCYGTQAAAAAYGYLILTS	294
MAELO	297	KNAKLAKOAKADAAREKARKLQ	318
GNS1	271	YLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSK	313
SUR4	287	YLLLFISFYINVYKRGKTKTSRVVKRAHGGVAAKVNNEYVNVDL	329
MAELO	295	YLLLFISFYIQSYKKKGKKTVKKESEVSGSVASGSSSTGVKTSN	337
GNS1	314	SKHI	317
SUR4	330	KNVPTPSPSPKPOHRRKR	347
MAELO	338	TKVSSRKA	345

# Figure 29

SCORES Init1: 83 Initn: 186 Opt: 271  
 Smith-Waterman score: 297; 28.5% identity in 242 aa overlap

	30	40	50	60	70	80
MAELO	YELVTGKSIDSFVFQEGVTPPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFILH					
					::  :::   :  :::   : : ::::	
HS1	STYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLLIVWLGPKYMRNKQPFSCRGILVVY					
	10	20	30	40	50	60
	90	100	110	120	130	140
MAELO	NFLLTIASGSLLLLFIEENLVPILARNGLFYAICDDGAWTQRLELLYYL--NYLVKYWELA					
	:   :   :   : : : :   : ::::     :     :					
HS1	NLGLTLLS--LYMFCELVTVGWEGKYNFFCQGTRTAGESDMKIIRVLWWYFYFSKLIEFM					
	70	80	90	100	110	120
	150	160	170	180	190	200
MAELO	DTVFLVLKK--KPLEFLHYFHH-SMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY-					
	:: :   : :    :      :   : :  :     :  :					
HS1	DTFFFILRKNNHQITVLHVYHHASMLNIWWFVMNWVPCGHSYFGATLNSFIHVLMYSSYG					
	130	140	150	160	170	180
	210	220	230	240	250	260
MAELO	MRSAAGVR--IWWKQYLTTLQIVQFVLDLGFIFYFCAYTYFAFTYFPWAPNVGKCAGTEGA					
	:  : ::  :   : :   ::    : :  :      :					
HS1	LSSVPSMRPYLWWKKYITQGQLLQFVLT-IQTSCGVI-----W-P-----CTFPLGW					
	190	200	210	220		230
	270	280	290	300	310	
MAELO	ALFGCGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHI					
	:   :             : : ::					
HS1	LYFQIGYMI SLIALFTNFYIQTYNKKGASRRKDHLKDHQNGSMAAVNGHTNSFSPLENNV					
	240	250	260	270	280	290
HS1	KPRKLRKDX					
	300					

# Figure 30

SCORES Init1: 88 Initn: 208 Opt: 272  
 Smith-Waterman score: 279; 28.2% identity in 266 aa overlap

	30	40	50	60	70	80
MAELO	QAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVIFGGRQIMKSQDAFKLKPLFI					
HS2	VNLYQEVMMKHADPRIQGYPLMGSPILLMTSILLTYVYFVLSLGPR-IMANRKPFQLRGFMI					
	10	20	30	40	50	60
	90	100	110	120	130	140
MAELO	LHNFLLTIASGSLLLJFTEN--LVPILAR-NGLFYAICDDGAWTQRLLELLYYLNYLVKYW					
HS2	VYNFSLVALSLYIVYEFLMSGWLSTYTWRCDPVDYSNSPEALRMVRVAWLFLFS---KF1					
	70	80	90	100	110	120
	150	160	170	180	190	
MAELO	ELADTVFLVLKFK--PLEFLHYFHHSMT---MVLCFVQLGGYTSVSWVPITLNLTVHVF					
HS2	ELMDTVIFILRKKGQVTFLHVFHHSVLPWSWWWGVKIAPGGMGSFHAM---INSSVHVI					
	130	140	150	160	170	
	200	210	220	230	240	
MAELO	MYYYMRSAGV---RIWWKQYLTTLQIVQFVL---DLGFIYF---CAYTYFAFTYFPW					
HS2	MYLYYGLSAFGPVAQPYLWWKKHMTAIQLIQFVLVSLHISQYYFMSSCNYPVILHLIW					
	180	190	200	210	220	230
	250	260	270	280	290	300
MAELO	APNVGKCGATEGAALFGCGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGS					
HS2	-----MYG---TIFFMLFSNFWYHSYTKGKRLPRALQONGAPGIAKVKAN					
		240	250	260	270	
	310					
MAELO	PKKPSKSKHI					
HS2	X					
	280					

# Figure 31

SCORES Init1: 88 Initn: 207 Opt: 223  
 Smith-Waterman score: 236; 30.4% identity in 191 aa overlap

	100	110	120	130	140	150
MAELO	LLLLFIENLVPILARNGLFYAICDDGAWTQRLLELLYYLNVLVKYWELADTVFLVLKKKP-					
				: : :  :          : : :  :		
MM2	IVYEFLMSGWLSTYTWRCDPIDFSNSPEALRMVRVAWLFMLSKVIELMDTVIFILRKKD					
	20	30	40	50	60	70
	160	170	180	190	200	209
MAELO	-LEFLHYFHHSMTIMVLCF---VQLGGYTSVSWVPITLNLTVHVFMYYYMRSAGV---					
	:           : : : :   :   :   :					
MM2	QVTFLHVFHHSVLPWSWWWGIKIAPGGMGSFHAM---INSSVHVVMYLYYGLSALGPVAQ					
	80	90	100	110	120	130
	210	220	230	240	250	260
MAELO	-RIWWKQYLTTLQIVQFVL---DLGFIYF---CAYTYFAFTYFPWAPNVGKCAGTEGAAL					
	:       : : :   : :       : :       : : :   : : :   : : :					
MM2	PYLWWFKHMTAIQLIQFVLVSLHISQYYFMPSCNYQYPVIIHLIW-----M					
	140	150	160	170		
	270	280	290	300	310	
MAELO	FGCGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKKPSKSKHI					
	:   : : :     : : : : : : : : : :   :   :					
MM2	YG---TIFFILFSNFWYHSYTKGKRLPRAVQQNGAPATTKVKAN					
	180	190	200	210		



# Figure 32

SCORES Init1: 51 Initn: 115 Opt: 168  
 Smith-Waterman score: 168; 30.4% identity in 115 aa overlap

	30	40	50	60	70	80
MAELO	YELVTGKSIDSFVFQEGVTPPLSTQREVAMWTITYFVWIFGGRQIMKSQDAFKLKPLFILH					
AI225632	NAFLDNMFGRPRDSRVRGWFLLDSTPLTFILTYLLSIWLGKYMKNRPALSLRGILTLY					
	20	30	40	50	60	70
	90	100	110	120	130	140
MAELO	NFLLTIASGSLLLFIENLVPILARNGLFYAICDD---GAWTQRLELLYYLNYLVKYWE					
AI225632	NLAITLLSAYMLVELI-----LSSWEGGYNLQCQNLDSEGEQDVRVAKVLVWYYFSLKVE					
	80	90	100	110	120	
	150	160	170	180	190	200
MAELO	LADTVFLVLKFK--PLEFLHYFHHSMTMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY					
AI225632	FLDTIFFVLRRKANQITFLHVYHHASMFNI					
	130	140	150			

## Figure 33

SCORES Frame: (3) Init1: 332 Initn: 332 Opt: 384  
40.3% identity in 144 aa overlap

	80	90	100	110	120	130
GLELO	LIVLAYLVTVFVGMQIMKNFERFEVKTFSLLHNFCLVSI SAYMCGGILYEAYQANYGL-F					
				: : :: :      : :: :::: :		
AI815960	LYNLGITLLSAYMLAELILSTWEGGYNLQC					
				10	20	30
	140	150	160	170	180	190
GLELO	ENADHTFKGLPMAKMIWLFYFSKIMEFVDTMIMVLKKNRQISFLHVVYHHSSIFTIWWL					
	:: ::	: :  ::	:	:  : ::: : :	: : : : : : : :	: : :
AI815960	QDLTSAGEADIRVAKVLWYYFYSKSVEFLDTIFFVLRKKTSQITFLHVVYHHASMFNIWWC					
	40	50	60	70	80	90
	200	210	220	230	240	250
GLELO	VTFVAPNGEAYFSAALNSFIHVIMYGYFLSAL-GFKQVSFIKFYITRSQMTQFCMMSVQ					
		::: :	:     : :	: : ::::	:	: : : :
AI815960	VLNWIPCGQSFFGPTLNSFIHILMYSYYGLSVFPSMHKYLWWKKYLTQAQLVQF					
	100	110	120	130	140	
	260	270	280	290	300	310
GLELO	SSWDMYAMKVLGRPGYPFFITALLWFYMWMTMLGLFYNFYRKNALAKQAKADAAKEKARK					

# Figure 34

SCORES Init1: 316 Initn: 384 Opt: 477  
 Smith-Waterman score: 477; 34.2% identity in 240 aa overlap

	50	60	70	80	90	100
GLELO	AQAKEYIPTIVHHTRGFLVAVESPLARELPLMNPFFHVLLIVLAYLVTVFVGMQIMKNFER					
	: :: :     :   :   :   :					
HS1	MEHFDASLSTYFKALLGPRDTRVKGWFI.LDNYIPTFICSVIYLLIVWLGPKYMRNKQP					
	10	20	30	40	50	

	110	120	130	140	150	159
GLELO	FEVKTFSLLLHNFCVLSISAYMCGGILYEAYQANYGLF-ENAAADHTFKGLPMAKMIWLFYF					
	: : ::   : :     : : : : :   : : : : : : : : :   :					
HS1	FSCRGILVVYNLGLTLLSLYMFCELVGTGVWEGKYNFFCQGTRTAGESDMKIIIRVLWWYYF					
	60	70	80	90	100	110

	160	170	180	190	200	210	219
GLELO	SKIMEFVDTMIMVLKKNRQISFLHVYHHSSIIFTIWWLVTFVAPNGEAYFSAALNSFIHV						
	: :   :   : : : :   :   :   :   :   :   :   :   :   :   :   :						
HS1	SKLIEFMDTFFFILRKNNHQITVLHVYHHASMLNIWWFVMNWVPCGHSYFGATLNSFIHV						
	120	130	140	150	160	170	

	220	230	240	250	260	270
GLELO	IMYGYFLSAL-GFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRPGYPFFITA					
	:   :   :   : : : : : :   :   : : :   : : : : :   : : :					
HS1	LMYSYGLSSVPSMRPYLWWKKYITQGQLLQFVLTIIQTS-----CGVIWPCTFPLGWLY					
	180	190	200	210	220	230

	280	290	300	310
GLELO	LLWFYMWMTMLGLFYNFYRK--NAKLAKQAKADAAKEKARKLQ			
	:   : : :   :   :   :   :   :			
HS1	FQIGYMISLIALFTNFYIQTYNKKGASRRKDHLKDHQNGSMAAVNGHTNSFSPLENNVKP			
	240	250	260	270

# Figure 35

SCORES Init1: 80 Initn: 114 Opt: 178  
 Smith-Waterman score: 178; 28.8% identity in 146 aa overlap

	140	150	160	170	180	190
GLELO	FENAADHTFKGLPMAKMIWLFYFSKIMEFVDTMIMVLKKNRQISFLHVYHHSSIFTIWW					
				::: :	:::         :::	
AC004050	DTIFIILRK--QKLIFLHWYHHITVLLYSW					
				10	20	
	200	210	220	230	240	250
GLELO	LVTfVAPNGEAYFSAALNSFIHVIMYGYFSLALGFKQVSFIKFYITRSQMTQFCMMSVQ					
	::	::	: :: :	:	: ::    :: :	
AC004050	YSYKDMVAGGGWF-MTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQITQMLMGCVV					
	30	40	50	60	70	80
	260	270	280	290	300	310
GLELO	SSWDMYAMKVLGRPGYPFFITALLW--FYMWTMLGLFYNFYRKN--AKLAKQAKADAAKE					
	: :  :	:	::	::: ::	: : :	: :   : :
AC004050	NYLVFCWMQ--HDQCHSHF-QNIFWSSLMYLSYLVLFCHFFFEAYIGKMRKTTKAEX					
	90	100	110	120	130	140
GLELO	KARKLQ					

# Figure 36

SCORES Init1: 288 Initn: 288 Opt: 399  
 Smith-Waterman score: 399; 34.6% identity in 211 aa overlap

	80	90	100	110	120	130
GLELO	LLIVLAYLVTVFVGMQIMKNFERFEVKTFSLHNFCLVSISAYMCGGILYEAYQANYGLF					
				:::      :     : :   : : :		
MM2	IVYNFSLVILSLYIVYEFLMSGWLSTYTWR					
				10	20	30
	140	150	160	170	180	190
GLELO	ENAAD--HTFKGLPMAKMIWLFYFSKIMEFVDTMIMVLKKNRQISFLHVVHHSSIFTIW					
	:		::	:::	::	::
MM2	CDPIDFSNSPEALRMVRVAWLFMLSKVIELMDTVIFILRKKDGQVTFHLHVFHHSVLPWSW					
	40	50	60	70	80	90
	200	210	220	230	240	250
GLELO	WLVTFVAPNGEAYFSAALNSFIHVIMYGYYFLSALGFKQVSFI--KFYITRSQMTQFCMM					
		:	:	:	:	:
MM2	WWGIKIAPGGMGSFHAMINSSVHVVMYLYYGLSALGPVAQPYLWWKKHMTAIQLIQFVLV					
	100	110	120	130	140	150
	260	270	280	290	300	309
GLELO	SVQSSWDMYAMKVLGRPGYPFFITALLWFYMWMTMLGLFYNF---YRKNALAKQAKADA					
	::	::	:	:	:	:
MM2	SLHIS-QYYFMPSCNYQ-YPVIIH-LIWMYGTIFFILFSNFWYHSYTKGKRLPRAVQQNG					
	160	170	180	190	200	
	310					
GLELO	AKEKARKLQ					
MM2	APATTKVKAN					
	210					

# Figure 37

SCORES Init1: 160 Initn: 227 Opt: 269  
 Smith-Waterman score: 269; 35.3% identity in 119 aa overlap

	50	60	70	80	90	100
GLELO	PTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLTVFVGMQIMKNFERFEVKTFS					
	: : : : :   : : : :   :     : : : :					
AI225632	NEVNAFLDNMFGPRDSRVRGWFLDLSYLPFTILTITYLLSIWLGKNKYMKNRPALSLRGIL					
	10	20	30	40	50	60
	110	120	130	140	150	160
GLELO	LLHNFCLVSISAYMCGGILYEAYQANYGLFENAADHTFKG-LPMAK-MIWLFIYFSKIMEF					
	:   : : : :       : : : : :   : : :   : :   : :   :       : :					
AI225632	TLYNLAITLLSAYMLVELILSSWEGGYNLQCQNLD SAGEGDVRVAKVLVW-YFYSKLVEF					
	70	80	90	100	110	120
	170	180	190	200	210	220
GLELO	VDTMIMVLKKNNRQISFLHVVHSSIFTIWWLVTFVAPNGEAYFSAALNSFIHVIMYGY					
	:     : : :     : :     :             : : : :					
AI225632	LDTIFFVLRKKANQITFLHVVHSHSMFNI					
	130	140	150			

# Figure 38

SCORES Init1: 64 Initn: 129 Opt: 233  
 Smith-Waterman score: 239; 23.7% identity in 279 aa overlap

	20	30	40	50	60	70
GLELO	FMDLATAIGVRAAPYVDPLEAALVAQAEKYIPTIVHHTRGFLVAVESPLAREL-----PL					
U97107	:   :: :    : : :     : MDTSMNFSRGLKMDLMQPYDFETFQDLRPF 10 20 30					
	80	90	100	110	120	129
GLELO	MNPFHV--LLIVLAYLVTVFVGMQIMKNFERFEVKTFSLHNFCLVSI SAYMCGGILYEA					
U97107	:: :   :     ::    : :    :   :: :   : :   :   :   : : LEEYWSSFLIVVVYLLLVVVGQTYMRTRKSFSLQRPILWSFFLAIFS--ILGTLRMWK 40 50 60 70 80					
	130	140	150	160	170	180
GLELO	YQAN---YGLFENAADHTFKGLPMAKMIW--LFYFSKIMEFVDTMIMVLKKNNRQISFL					
U97107	:: :    :: : : : :      :    :: :    :: :   :   : FMATVMFTVGLKQTVCFAIYTDDAVVRF-WSFLFLLSKVVELGDTAFIILRK--RPLIFV 90 100 110 120 130 140					
	190	200	210	220	230	240
GLELO	HVVYHSSI--FTIWVLVTFVAPNGEAYFSAALNSFIHVIMYGYFFLSALGFKQVSFIKFY					
U97107	::    : :     : : : :   :   :       :   :   : : : HWYHHSTVLLFTSFGYKNKV-PSGGWFMT--MNFGVHSVMTYYTMTKAAKLKHPNLLPMV 150 160 170 180 190 200					
	250	260	270	280	290	
GLELO	ITRSQMTQFCMMSVQSSWDMYAMKVLG--RPGYPFFITALLWFYMWMTMLGLFYN--FYRK					
U97107	:   : : : : : :      : :   : : : :   : : :   ITSLQILQMVLTIFGILNYIWRQEKGCHTTTEHFFWSFMLYGTYFILFAHFFHRAYLRP 210 220 230 240 250 260					
	300	310				
GLELO	NAKLAKQAKADAAKEKARKLQ					
U97107	:: :  :::					
		270				
		KGKVASKSQ				

# Figure 39

SCORES Init1: 100 Initn: 205 Opt: 271  
Smith-Waterman score: 271; 30.7% identity in 218 aa overlap

	60	70	80	90	100	110
GLELO	TRGFLVAVESPLARELPLMNPFFHVLIVLAYLVTVFVGMQIMKNFERFEVKTFSLLHNFC					
				: :	: :	: :
U68749	ATHGPKNFPDAEGRKFFADHFDVTIQASILYMVVVFGTKWFMNRQPPQLTIPLNIWNFI					
(F56H11.4)	30	40	50	60	70	80

	120	130	140	150	160
GLELO	LVSISAYMCGGILYEAYQ--ANYGL---FENAADHTFKGLPMAKMIWLFYFSKIMEFVD				
	::	:	:	:	:::
U68749	LAAFSIAGAVKMTPEFFGTIANKGIVASYCKVDFDT-KG-ENGWVWLFMASKLFELVD				
(F56H11.4)	90	100	110	120	130

	170	180	190	200	210	220
GLELO	MIMVLKKNRQISFLHVVYHHSSIFTIWWLVTFVAPNGEAYFSAALNSFIHVIMYGYF					
	:::	:		:	:	:
U68749	IFLVLRK--RPLMFLHWYHHILTMIAWYSHPLTP-GFNRYGIYLNFFVHAFMYSYFL					
(F56H11.4)	150	160	170	180	190	

	230	240	250	260	270	280
GLELO	ALGFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRP-GYPFFITALLWFYMW					
	:::	:		:	::	:
U68749	SMKIRVPGFIAQAITSQIVQFIISCAVLAHLGYLMHFTNANCDFEPSVFKLAVFMD					
(F56H11.4)	200	210	220	230	240	250

	290	300	310
GLELO	LGLFYNFYRFNAKLAKQAKADAAKEKARKLQ		
	:	:	
U68749	LALFVNFFLQSYVLRGGKDKYKAVPKKKNN		
(F56H11.4)	260	270	280



# Figure 40

SCORES Init1: 189 Initn: 264 Opt: 358  
Smith-Waterman score: 358; 28.7% identity in 296 aa overlap

	10	20	30	40	50	59
MAELO	MAAAILDKVNFGIDQPPFGIKLDTYFAQAYELVTGKSIDSFVFQEGVTPPLSTQREVAMW-T					
	::: : : :  : : : : :  :  : : : : : : :					
U68749	MAQHPLVQRLLDVKFDT---KRFVAIATHGPKNFPDAEGRKFFADHFDVTIQAS					
(F56H11.4)	10	20	30	40	50	

	60	70	80	90	100	110
MAELO	ITYFVVIFGGRQIMKSQDAFKLK-PLFILHNFLLTIASGSLLLLFIE NLVPILARNGLFY					
	:   :  : : : : :  :       :  :  : : : : :  :  :					
U68749	ILYMVVVFGTKWFMNRNQPFQLTIPLNIW-NFILAAFSIAGAVKMTPEFFGTIANKGIVA					
(F56H11.4)	60	70	80	90	100	110

	120	130	140	150	160	170
MAELO	AICDDGAWTQRLELLYYLNYLV-KYWELADTVFLVLKKKPLEFLHYFHHSM TMVLCFVQL					
	:   : : : : : : :  : :   :   :   :   :   :  :  :  : :					
U68749	SYCKVFDFTKGENGYVWVLFMASKLFELVDITFLVLRKRPLMFLHWYHHIL TMIYAWYSH					
(F56H11.4)	120	130	140	150	160	170

	180	190	200	210	220	230
MAELO	GGYTSVSWVPITLNLTVHVFMY-YYMRSAAAGVRI--WWKQYLTTLQIVQFVLDLGF IYF					
	: :    :   :   :   :   :  :  : :  :   :   :  : : : :					
U68749	PLTPGFNRYGIYLN FVVHAFMYSYYFLRSMK-IRVPGFIAQAITS LQIVQFIISCAVL AH					
(F56H11.4)	180	190	200	210	220	

	240	250	260	270	280	
MAELO	CAYT-YFAFTYFPWAPNVGK CAGTEGAALFGCGLLSSYLLLFINFYRITY-----NAKAK					
	:  : : : : :    :  : :     :  :  :  :  :					
U68749	LGYLMHFTNANCD FEPSVFKLA-----VF---MDTTYLALFVNFFLQSYVLRGGKDKYK					
(F56H11.4)	230	240	250	260	270	280

	290	300	310
MAELO	AAKERGSNFTPKTVKSGGSPKKPSKSKHI		
	: : :		
U68749	AVPKKKNN		
(F56H11.4)			

# Figure 41

SCORES Init1: 77 Initn: 155 Opt: 264  
 Smith-Waterman score: 264; 27.2% identity in 206 aa overlap

	40	50	60	70	80	90
GLELO	AALVAQAKEYIPTIVHHTRGFLVAVESPLARELPLMNPFHVLLIVLAYLVTVFVGMQIMK					
				:      :	:::   ::: :	
DM1	PTKMINMDISVTPNYSYIFDFENDFIHQTRKWMLENWTWVFYYCGIYMLVIFGGQHFMQ					
	10	20	30	40	50	60

	100	110	120	130	140	150
GLELO	NFERFEVKTFSLHNFCLVSIAYMCGGILYEAYQA--NYGLFENAADHTF--KGLPMAK					
	::: ::    : :  : :   :: :   ::: :: : :					
DM1	NRPRFQLRGPLIIWNTLLAMFSIMGAARTAPELIHVLRLHYGLFHSVCVPSYIEQDRVCGF					
	70	80	90	100	110	120

	160	170	180	190	200	210
GLELO	MIWLFYFSKIMEFVDTMIMVLKKNRQISFLHVYHHSSIFTIWWLVTFVAPNGEAYFSAA					
	:  :  :  ::: :  : :         ::  :::: ::   : :					
DM1	WTWLFVLSKLPGLGDTIFIVLRK--QPLIFLHWYHHITVLIYSWF-SYTEYTSSARWFIV					
	130	140	150	160	170	180

	220	230	240	250	260	270
GLELO	LNSFIHVIMYGYFLSALGFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRPGY					
	:  :  :  :   :   :   ::     : : : : :   : :					
DM1	MNYCVHSVMSYYSYALKAAARFNPPRFISMIITSLQLAQMIIGCAINWANGFLKTHGTXSC					
	190	200	210	220	230	240

	280	290	300	310
GLELO	PFFITALLWFYMWMTMLGLFYNFYRKNKAKLAKQAKADAAKEKARKLQ			
DM1	HISQRNINLSIAMYSSYFVLFARFFYKAYLAPGGHKSRMA			
	250	260	270	280

\_\_\_\_\_

SCORES    Init1: 181    Initn: 279    Opt: 328  
Smith-Waterman score: 328;    30.0% identity in 237 aa overlap

[illegible]

Figure 43

1	ATGGAACATT	TTGATGCATC	ACTTAGTACC	TATTTCAAGG	CATTGCTAGG
51	CCCTCGAGAT	ACTAGAGTAA	AAGGATGGTT	TCTTCTGGAC	AATTATATAC
101	CCACATTTAT	CTGCTCTGTC	ATATATTTAC	TAATTGTATG	GCTGGGACCA
151	AAATACATGA	GGAATAAACA	GCCATTCTCT	TGCCGGGGGA	TTTTAGTGGT
201	GTATAACCTT	GGACTCACAC	TGCTGTCTCT	GTATATGTTC	TGTGAGTTAG
251	TAACAGGAGT	ATGGGAAGGC	AAATACAAC	TCTTCTGTCA	GGGCACACGC
301	ACCGCAGGAG	AATCAGATAT	GAAGATTATC	CGTGTCTCT	GGTGGTACTA
351	CTTCTCCAAA	CTCATAGAAT	TATATGGACAC	TTTCTTCTTC	ATCCTGCGCA
401	AGAACAACCA	CCAGATCACG	GTCCTGCACG	TCTACCACCA	TGCCTCGATG
451	CTGAACATCT	GGTGGTTTGT	GATGAACTGG	GTCCCCCTGCG	GCCACTCTTA
501	TTTTGGTGCC	ACACTTAATA	GCTTCATCCA	CGTCCTCATG	TACTCTTACT
551	ATGGTTTGTC	GTCAGTCCCT	TCCATGCGTC	CATACCTCTG	GTGGAAGAAG
601	TACATCACTC	AGGGGCAGCT	GCTTCAGTTT	GTGCTGACAA	TCATCCAGAC
651	CAGCTGCGGG	GTCATCTGGC	CGTGCACATT	CCCTCTTGGT	TGGTTGTATT
701	TCCAGATTGG	ATACATGATT	TCCCTGATTG	CTCTCTTCAC	AACTTCTAC
751	ATTCAGACCT	ACAACAAGAA	AGGGGCCTCC	CGAAGGAAAG	ACCACCTGAA
801	GGACCACCAG	AATGGGTCCA	TGGCTGCTGT	GAATGGACAC	ACCAACAGCT
851	TTTCACCCCT	GGAAAACAAT	GTGAAGCCAA	GGAAGCTGCG	GAAGGATTGA
901	AGTCAAAGAA	TTGA			

## Figure 44

1 MEHFDASLST YFKALLGPRD TRVKGWFLLD NYIPTFICSV IYLLIVWLGP  
51 KYMRNKQPFS CRGILVVYNL GLTLLSLYMF CELVTGVWEG KYNFFCQGTR  
101 TAGESDMKII RVLWYYYFSK LIEFMDTFFF ILRKNNHQIT VLHVYHHASM  
151 LNIWWFVMNW VPCGHSYFGA TLNSFIHVLM YSYYGLSSVP SMRPYLWWKK  
201 YITQGQLLQF VLTIIQTSCG VIWPCTFPLG WLYFQIGYMI SLIALFTNFY  
251 IQTYNKKGAS RRKDHLKDHQ NGSMAAVNGH TNSFSPLENN VKPRKLRKD\*

Figure 45

Host (plasmid)	334(pYX242)	334(pRAE-58-A1)	334(pYX242)	334(pRAE-58-A1)
Added substrate	25 $\mu$ M GLA	25 $\mu$ M GLA	25 $\mu$ M AA	25 $\mu$ M AA
Fatty acid	% total fatty acid	% total fatty acid	% total fatty acid	% total fatty acid
C18:3n-6	4.40	2.71	0.03	0.04
<b>C20:3n-6</b>	0.09	<b>(50.34%)* 2.75</b>	0.02	0.02
C20:4n-6			7.84	3.97
<b>C22:4n-6</b>			ND	<b>(23.37%)* 1.21</b>
C16:1n-7	41.11	34.72	41.49	35.07
C18:1n-7	1.85	<b>11.33</b>	2.01	<b>11.57</b>
C20:1n-7	0.04	<b>1.48</b>	0.04	<b>1.62</b>
C18:1n-9	15.60	15.66	15.16	14.57
C20:1n-9	0.06	<b>0.22</b>	0.06	<b>0.23</b>
C18:1n-5	0.11	<b>0.62</b>	0.12	<b>0.58</b>
Total Lipid	370	969	359	514

\*% conversion=product/(substrate+product)

Figure 46

```
1  ATGGCTCAGC ATCCGCTCGT TCAACGGCTT CTCGATGTCA AATTCGACAC
51  GAAACGATTT GTGGCTATTG CTACTCATGG GCCAAAGAAT TTCCCTGACG
101 CAGAAGGTCG CAAGTTCTTT GCTGATCACT TTGATGTTAC TATTCAGGCT
151 TCAATCCTGT ACATGGTCGT TGTGTTTCGGA AAAAAATGGT TCATGCGTAA
201 TCGTCAACCA TTCCAATTGA CTATTCCACT CAACATCTGG AATTTCATCC
251 TCGCCGCATT TTCCATCGCA GGAGCTGTCA AAATGACCCC AGAGTTCTTT
301 GGAACCATTG CCAACAAAGG AATTGTCGCA TCCTACTGCA AAGTGTTTGA
351 TTTCACGAAA GGAGAGAATG GATACTGGGT GTGGCTCTTC ATGGCTTCCA
401 AACTTTTCGA ACTTGTGAC ACCATCTTCT TGGTTCTCCG TAAACGTCCA
451 CTCATGTTCC TTCCTGGTA TCACCATATT CTCACCATGA TCTACGCCTG
501 GTACTCTCAT CCATTGACCC CAGGATTCAA CAGATACGGA ATTTATCTTA
551 ACTTTGTCGT CCACGCCTTC ATGTACTCTT ACTACTTCCT TCGCTCGATG
601 AAGATTCGCG TGCCAGGATT CATCGCCCAA GCTATCACAT CTCTTCAAAT
651 CGTTCAATTC ATCATCTCTT GCGCCGTTCT TGCTCATCTT GGTATCTCA
701 TGCACTTCAC CAATGCCAAC TGTGATTTTC AGCCATCAGT ATTCAAGCTC
751 GCAGTTTTCA TGGACACAAC ATACTTGGCT CTTTTCGTCA ACTTCTTCCT
801 CCAATCATAT GTTCTCCGCG GAGGAAAAGA CAAGTACAAG GCAGTGCCAA
851 AGAAGAAGAA CAACTAA
```

## Figure 47

1 MAQHPLVQRL LDVKFDTKRF VAIATHGPKN FPDAEGRKFF ADHFDVTIQA  
51 SILYMVVVFG TKWFMRNRQP FQLTIPLNIW NFILAAFSIA GAVKMTPEFF  
101 GTIANKGIVA SYCKVFDFTK GENGYWVWLF MASKLFELVD TIFLVLRKRP  
151 LMFLHWYHHI LTMIYAWYSH PLTPGFNRYG IYLNFVVHAF MYSYYFLRSM  
201 KIRVPGFIAQ AITSLQIVQF IISCAVLAHL GYLMHFTNAN CDFEPSVFKL  
251 AVFMDTTYLA LFVNFFLQSY VLRGGKDKYK AVPKKKNN



Figure 48

Host (plasmid)	334(pYX242)	334(pRET-21)	334(pRET-22)
Added Substrates	50 $\mu$ M GLA + 50 $\mu$ M AA	50 $\mu$ M GLA + 50 $\mu$ M AA	50 $\mu$ M GLA + 50 $\mu$ M AA
Fatty Acid	%total fatty acid	%total fatty acid	%total fatty acid
C16:0	9.22	12.46	9.9
C16:1	0.09	0.18	0.13
C18:0	1.46	2.41	1.49
C18:1n-9	4.03	4.92	3.91
C18:3n-6	10.02	11.89	8.69
C20:3n-6	<b>(1.28%)* 0.13</b>	<b>(11.1%)* 1.48</b>	<b>(19.4%)* 2.09</b>
C20:4n-6	46.98	28.87	35.25
C22:4n-6	0	0	0
Total lipid (mg)	212	174	187
*% conversion=product/(substrate+product)			

Figure 49

1	ATGAACATGT	CAGTGTTGAC	TTTACAAGAA	TATGAATTCTG	AAAAGCAGTT
51	CAACGAGAAT	GAAGCCATCC	AATGGATGCA	GGAAAACCTGG	AAGAAATCTT
101	TCCTGTTTTT	TGCTCTGTAT	GCTGCCTTTA	TATTCGGTGG	TCGGCACCTA
151	ATGAATAAAC	GAGCAAAGTT	TGAACTGAGG	AAGCCATTAG	TGCTCTGGTC
201	TCTGACCCTT	GCAGTCTTCA	GTATATTCTG	TGCTCTTCGA	ACTGGTGCTT
251	ATATGGTGTA	CATTTTGATG	ACCAAAGGCC	TGAAGCAGTC	AGTTTGTGAC
301	CAGGGTTTTT	ACAATGGACC	TGTCAGCAAA	TTCTGGGCTT	ATGCATTTGT
351	GCTAAGCAAA	GCACCCGAAC	TAGGAGATAC	AATATTTCATT	ATTCTGAGGA
401	AGCAGAAGCT	GATCTTCCTG	CACTGGTATC	ACCACATCAC	TGTGCTCCTG
451	TACTCTTGGT	ACTCCTACAA	AGACATGGTT	GCCGGGGGAG	GTTGGTTCAT
501	GACTATGAAC	TATGGCGTGC	ACGCCGTGAT	GTACTCTTAC	TATGCCTTGC
551	GGGCGGCAGG	TTTCCGAGTC	TCCCGGAAGT	TTGCCATGTT	CATCACCTTG
601	TCCCAGATCA	CTCAGATGCT	GATGGGCTGT	GTGGTTAACT	ACCTGGTCTT
651	CTGCTGGATG	CAGCATGACC	AGTGTCACTC	TCACTTTCAG	AACATCTTCT
701	GGTCCTCACT	CATGTACCTC	AGCTACCTTG	TGCTCTTCTG	CCATTTCTTC
751	TTTGAGGCCT	ACATCGGCAA	AATGAGGAAA	ACAACGAAAG	CTGAATAG

## Figure 50

1 MNMSVLTLQE YEFKQFNEN EAIQWMQENW KKSFLFSALY AAFIFGGRHL  
51 MNKRAKFELR KPLVLWSTL AVFSIFGALR TGAYMVYILM TKGLKQSVCD  
101 QGFYNGPVSK FWAYAFVLSK APELGDITFI ILRKQKLIFL HWYHHITVLL  
151 YSWYSYKDMV AGGGWFMTMN YGVHAVMYSY YALRAAGFRV SRKFAMFITL  
201 SQITQMLMGC VVNYLVFCWM QHDQCHSHFQ NIFWSSLMYL SYLVLFCHFF  
251 FEAYIGMRK TTKAE\*

**Figure 51**

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58
Substrate	GLA	GLA	AA	AA	STA	STA	EPA	EPA	OA	OA	ALA	ALA	ALA	ALA
Concentration	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM
% total lipid														
C18:1n-9	18.75	12.96	16.95	12.76	16.06	14.48	19.55	13.78	29.42	23.06	ND	ND	14.58	
C18:1n-7	2.00	18.49	2.30	18.70	1.45	13.26	2.75	13.62	2.50	16.42	1.87	13.76		
C18:1n-5	0.29	1.63	0.24	1.61	0.33	0.97	0.32	1.10	0.30	1.64	0.28	1.18		
C18:3n-6	4.61	2.02	0.04	0.04	0.02	0.09	0.06	0.05	0.02	0.05	0.01	0.01		
C18:3n-3	0.02	0.08	0.02	0.07	0.01	0.03	0.04	0.05	0.02	0.08	14.74	14.08		
C18:4n-3	ND	ND	ND	ND	7.01	2.65	ND	ND	ND	ND	ND	ND		
C20:1n-9	0.10	0.77	0.11	0.70	0.15	0.55	0.15	0.46	0.27	2.25	0.10	0.57		
C20:1n-7	0.08	8.45	0.10	8.06	0.04	3.95	0.14	4.48	0.10	(8.9%/9.35)	0.06	3.53		
C20:3n-6	0.17	(78.3%/7.29)	0.01	0.07	ND	0.04	ND	ND	ND	ND	ND	ND		
C20:3n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	0.41	(30.4%/6.15)		
C20:4n-6	ND	ND	22.07	8.40	ND	0.07	ND	ND	ND	ND	ND	ND		
C20:4n-3	ND	ND	ND	ND	0.25	(79.2%/10.07)	ND	ND	ND	ND	ND	ND		
C20:5n-3	ND	ND	0.01	ND	0.18	0.08	8.21	2.63	ND	0.02	ND	ND		
C22:4n-6	ND	ND	ND	(42.7%/6.26)	ND	ND	ND	ND	ND	ND	ND	ND		
C22:5n-3	ND	ND	ND	ND	ND	0.18	ND	(71.7%/6.66)	ND	ND	ND	ND		
Total Lipid	158	104	144	112	324	209	178	94	148	87	243	315		

(% conversion) = product/(substrate + product)  
 ND= not detected

**Figure 52**

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	pRAE-58
Substrate	GLA	GLA	GLA	GLA	AA	AA	AA	AA	AA	AA	EPA	EPA	EPA	EPA	EPA	EPA	EPA	EPA	EPA
Concentration	25μM	25μM	100μM	100μM	25μM	25μM	100μM	100μM	25μM	25μM	100μM	100μM	25μM	25μM	100μM	100μM	100μM	100μM	100μM
% total lipid																			
C18:1n-9	23.82	21.49	18.49	17.41	22.09	19.23	17.45	18.44	24.78	21.28	19.42	18.85							
C18:1n-7	2.52	18.35	1.71	11.82	2.54	18.77	1.78	12.67	2.64	19.48	1.79	12.40							
C18:1n-5	0.15	1.13	0.10	0.54	0.15	1.23	0.10	0.63	0.15	1.18	0.09	0.62							
C18:3n-6	6.10	2.38	23.30	14.46	0.04	0.02	0.04	0.02	0.04	0.02	0.01	0.01							
C20:1n-9	0.08	0.83	0.05	0.48	0.10	1.18	0.04	0.56	0.10	1.30	0.06	0.63							
C20:1n-7	0.10	5.75	0.07	3.09	0.11	9.49	0.05	3.62	0.10	9.94	0.08	4.07							
C20:3n-6	0.15	(62.4%)3.95	0.31	(39.8%)9.56	0.02	ND	ND	0.04	ND	0.02	0.01	0.01							
C20:4n-6	ND	ND	0.01	ND	11.76	7.68	28.39	21.02	0.02	0.02	ND	0.01							
C20:5n-3	ND	ND	ND	ND	0.03	0.02	0.10	0.07	4.79	2.04	26.47	13.69							
C22:4n-6	ND	ND	ND	ND	ND	(27.5%)2.91	0.01	(15.7%)3.90	ND	ND	0.00	ND							
C22:5n-3	ND	ND	ND	ND	ND	ND	ND	0.03	0.02	(70.3%)4.82	0.04	(45.7%)11.50							
Total Lipid	230	419	590	576	249	332	1014	961	372	390	1323	1065							

(% conversion) = product/(substrate + product)

ND= not detected

Figure 53

A

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242	pRAE-58	PYX242
Substrate	PA	PA	SA	SA	ARA	ARA	BA	BA	PTA	PTA	OA	OA	EA	EA	EA	EA	EA	EA	EA
Concentration	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM
% total lipid																			
C16:0	24.17	17.23	11.22	7.90	7.74	7.98	7.62	7.11	17.28	11.04	16.06	12.76	14.37	11.98					
C16:1n-7	39.83	33.83	30.62	20.56	21.61	19.81	21.34	22.89	50.06	39.43	40.95	30.06	43.34	29.51					
C16:1n-5	0.30	0.74	0.29	0.58	0.17	0.47	0.18	0.59	0.38	0.80	0.34	0.68	0.37	0.71					
C18:0	1.90	1.50	35.82	38.10	1.12	0.89	1.03	0.88	1.90	1.44	1.82	1.43	1.51	1.23					
C18:1n-9	15.36	14.11	11.52	10.88	8.29	10.03	8.09	10.25	14.55	13.86	20.12	21.37	14.12	15.15					
C18:1n-7	1.36	11.44	0.90	8.72	0.69	8.51	0.69	8.58	1.30	12.76	1.30	13.79	1.21	12.66					
C18:1n-5	0.11	0.78	0.08	0.69	0.08	0.54	0.06	0.61	0.19	0.76	0.10	0.90	0.15	0.84					
C20:0	0.15	0.17	0.09	0.12	52.07	41.48	ND	ND	ND	ND	ND	ND	0.17	0.23					
C20:1n-9	0.09	0.45	0.05	0.30	0.03	ND	0.06	0.28	0.05	0.38	0.18	0.58	7.47	10.97					
C20:1n-7	0.20	2.84	ND	1.52	0.05	1.43	0.14	1.60	0.07	2.76	0.12	2.08	ND	2.30					
C22:0	0.43	0.56	0.29	0.22	0.31	0.19	52.91	38.43	ND	ND	ND	ND	ND	0.32					
C24:0	0.59	1.39	0.36	0.85	0.45	0.71	0.53	1.14	0.45	1.63	0.66	1.02	0.56	0.79					
Total Lipid	297	272	573	542	558	846	585	519	464	295	306	448	309	648					

ND = not detected

# Figure 53

B

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58
Substrate	LA	LA	GLA	GLA	DGLA	DGLA	AA	AA	ADA	ADA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
	% total lipid									
C18:1n-9	15.27	16.83	14.85	15.58	13.62	16.24	15.08	15.64	16.18	13.98
C18:1n-7	1.21	13.53	1.22	11.80	1.16	12.63	1.18	11.70	1.30	10.67
C18:1n-5	0.13	0.95	0.20	0.73	0.12	0.72	0.14	0.59	0.12	0.70
C18:2n-6	4.09	4.85	0.09	0.07	0.07	0.04	0.04	0.04	0.03	0.07
C18:3n-6	ND	ND	4.66	2.33	ND	ND	ND	ND	ND	ND
C20:1n-9	0.07	2.60	0.07	0.33	0.07	0.33	0.04	0.27	0.08	0.33
C20:1n-7	0.10	0.18	0.14	1.65	0.08	1.68	0.12	1.58	0.12	1.85
C20:2n-6	ND	(13.2%)0.74	ND	ND	ND	ND	ND	ND	ND	ND
C20:3n-6	ND	ND	ND	(51.4%)2.46	6.37	7.86	ND	0.03	ND	ND
C20:4n-6	ND	ND	ND	ND	ND	0.09	6.49	5.77	ND	ND
C22:4n-6	ND	ND	ND	ND	ND	ND	ND	(27.1%)2.14	10.91	15.57
C24:0	0.59	1.61	0.64	1.12	0.69	0.79	0.52	0.77	0.54	1.26
Total Lipid	333	373	260	392	260	672	553	690	706	440

C

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58
Substrate	ALA	ALA	STA	STA	EPA	EPA	DPA	DPA		
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM		
	% total lipid									
C18:1n-9	17.21	17.36	16.85	17.71	16.45	16.93	17.08	16.68	18.36	18.77
C18:1n-7	1.29	12.20	1.15	11.38	1.23	11.48	1.33	11.61	1.46	13.72
C18:1n-5	0.14	0.68	0.12	0.57	0.12	0.54	0.12	0.63	0.13	0.79
C18:3n-3	4.42	3.61	ND	0.03	ND	0.03	ND	0.03	ND	0.03
C18:4n-3	ND	0.13	3.04	1.38	ND	0.13	ND	0.13	ND	0.17
C20:1n-9	0.09	0.33	0.11	0.34	0.05	0.31	0.09	0.30	0.13	0.34
C20:1n-7	0.13	1.55	0.05	1.38	0.23	1.89	0.18	1.73	0.15	1.76
C20:3n-3	0.06	(22.2%)1.03	ND	ND	ND	0.11	ND	ND	ND	ND
C20:4n-3	ND	ND	0.06	(61.9%)2.24	ND	ND	ND	ND	ND	ND
C20:5n-3	ND	ND	0.05	0.05	7.43	4.88	ND	ND	0.07	ND
C22:4n-3	ND	ND	ND	0.39	ND	ND	ND	ND	ND	ND
C22:5n-6	ND	ND	ND	ND	ND	ND	0.28	0.41	ND	ND
C22:5n-3	ND	ND	ND	ND	ND	(39.5%)3.19	3.99	5.94	ND	ND
C24:0	0.43	0.73	0.33	0.73	0.45	0.84	0.64	1.07	0.68	0.77
C24:5n-3	ND	ND	ND	ND	ND	0.08	ND	0.06		ND
Total Lipid	696	729	911	710	719	703	602	642	397	684

(% conversion) = product/(substrate + product)

ND= not detected

**Figure 54**

```
1  ATGGAGCAGC TGAAGGCCTT TGATAATGAA GTCAATGCTT TCTTGGACAA
51 CATGTTTGGG CCACGAGATT CTCGAGTTCG CGGGTGGTTC CTGCTGGACT
101 CTTACCTTCC CACCTTCATC CTCACCATCA CGTACCTGCT CTCGATATGG
151 CTGGGTAACA AGTACATGAA GAACAGGCCT GCTCTGTCTC TCAGGGGCAT
201 CCTCACCTTG TATAACCTCG CAATCACACT TCTTTCTGCG TATATGCTGG
251 TGGAGCTCAT CCTCTCCAGC TGGGAAGGAG GTTACAACCT GCAGTGTGAG
301 AATCTCGACA GTGCAGGAGA AGGTGATGTC CGGGTAGCCA AGGTCTTGTG
351 GTGGTACTAC TTCTCCAAAC TAGTGGAGTT CCTGGACACG ATTTTCTTTG
401 TTCTACGAAA AAAGACCAAT CAGATCACCT TCCTTCATGT CTATCACCAC
451 GCGTCCATGT TCAACATCTG GTGGTGTGTT TTGAACTGGA TACCTTGTGG
501 TCAAAGCTTC TTTGGACCCA CCCTGAACAG CTTTATCCAC ATTCTCATGT
551 ACTCCTACTA CGGCCTGTCT GTGTTCCCGT CCATGCACAA GTACCTTTGG
601 TGGAAGAAGT ACCTCACACA GGCTCAGCTG GTGCAGTTCG TACTCACCAT
651 CACGCACACG CTGAGTGCCG TGGTGAAGCC CTGTGGCTTC CCCTTTGGCT
701 GTCTCATCTT CCAGTCTTCC TATATGATGA CGCTGGTCAT CCTGTTCTTA
751 AACTTCTATA TTCAGACATA CCGGAAAAAG CCAGTGAAGA AAGAGCTGCA
801 AGAGAAAGAA GTGAAGAATG GTTTCCCCAA AGCCCACTTA ATTGTGGCTA
851 ATGGCATGAC GGACAAGAAG GCTCAATAA
```



## Figure 55

1 MEQLKAFDNE VNAFLDNMFG PRDSRVRGWF LLDSYLPTEI LTITYLLSIW  
51 LGNKYMKNRP ALSLRGILT YNLAITLLSA YMLVELILSS WEGGYNLQCQ  
101 NLDSAGEGDV RVAKVLWWYY FSKLVEFLDT IFFVLRKKTN QITFLHVVHH  
151 ASMFNIWWCV LNWIPCGQSF FGPTLNSFIH ILMYSYYGLS VFPSMHKYLW  
201 WKKYLTQAQL VQFVLTITHT LSAVVKPCGF PFGCLIFQSS YMMTLVILFL  
251 NFYIQTYRKK PVKKELQEKE VKNGFPAHL IVANGMTDKK AQ\*

Figure 56

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242
Substrate	GLA	GLA	AA	AA	ADA	ADA	ADA	STA	STA	EPA	EPA	EPA	DPA	DPA	DPA	DPA	DPA	DPA	DPA
Concentration	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM	25µM
% total lipid																			
C18:1n-9	15.94	14.16	12.30	15.67	11.77	11.41	14.81	17.92	15.91	16.33	15.04	14.63							
C18:1n-7	1.25	1.21	1.10	1.50	1.13	1.18	1.19	1.38	1.33	1.49	1.37	1.38							
C18:3n-6	4.53	4.21	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND							
C18:4n-3	ND	ND	ND	ND	ND	ND	2.78	2.70	ND	ND	ND	ND							
C20:1n-7	ND	ND	ND	ND	ND	0.32	ND	0.03	ND	0.05	ND	ND							
C20:3n-6	0.10	0.37	ND	ND	ND	ND	ND	0.05	ND	ND	ND	ND							
C20:4n-6	ND	ND	11.44	5.55	ND	ND	ND	ND	ND	ND	ND	ND							
C20:4n-3	ND	ND	ND	ND	ND	ND	(14%)0.44	ND	ND	ND	ND	ND							
C20:5n-3	ND	ND	ND	ND	ND	ND	ND	9.68	3.02	ND	ND	ND							
C22:4n-6	ND	ND	ND	(10.4%)0.64	20.41	23.61	ND	ND	ND	ND	ND	ND							
C22:4n-3	ND	ND	ND	ND	ND	ND	(42.3%)0.33	ND	ND	ND	0.57	0.57							
C22:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(32.7%)1.47	7.87	4.88							
C24:4n-6	ND	ND	ND	(62.6%)1.07	ND	(9.2%)2.4	ND	ND	ND	ND	ND	ND							
C24:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	(82.8%)7.06	ND	(43.9%)3.82								
Total Lipid	208	126	115	189	158	149	124	433	221	271	127	126							

(% conversion ) = product/(substrate + product)  
 ND = not detected



Figure 57

B

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84
Substrate	LA	LA	GLA	GLA	DGLA	DGLA	AA	AA	ADA	ADA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
	% total lipid									
C18:1n-9	12.30	16.12	15.63	16.28	14.28	13.77	16.21	15.04	15.38	12.94
C18:1n-7	1.34	1.87	1.69	1.90	1.41	1.61	1.61	1.62	1.51	1.47
C18:2n-6	2.67	3.61	0.17	0.20	0.24	0.21	0.09	0.09	0.06	0.14
C18:3n-6	ND	ND	2.03	2.49	ND	ND	ND	ND	ND	ND
C20:3n-6	ND	ND	ND	(14.7%)0.43	10.59	10.73	ND	ND	ND	ND
C20:4n-6	ND	ND	ND	ND	ND	ND	14.03	5.27	ND	ND
C22:4n-6	ND	ND	ND	ND	ND	ND	ND	(8.7%) 0.5	11.44	16.60
C24:0	0.79	1.00	1.08	1.16	1.30	0.87	0.87	0.72	0.77	1.18
C24:4n-6	ND	ND	ND	ND	ND	ND	ND	(43.8%)0.39	ND	(7.3%)1.3
C24:5n-6	ND	ND	ND	ND	ND	ND	ND	0.38	ND	ND
Total Lipid	85	87	88	79	107	98	208	212	304	122

C

Host	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84
Substrate	ALA	ALA	STA	STA	EPA	EPA	DPA	DPA		
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM		
	% total lipid									
C18:1n-9	16.69	16.38	18.24	15.95	14.07	15.16	16.05	15.06	17.47	17.15
C18:1n-7	1.37	1.43	1.71	1.40	1.37	1.47	1.67	1.51	1.75	1.73
C18:2n-6	0.08	0.08	0.12	0.04	0.13	0.06	0.11	0.18	0.13	0.15
C18:3n-3	4.47	4.28	ND	ND	ND	ND	ND	ND	ND	ND
C18:4n-3	ND	ND	2.28	2.39	ND	ND	ND	ND	ND	ND
C20:3n-3	(1.3%)0.06	(3.6%)0.16	ND	ND	ND	0.26	ND	ND	ND	0.12
C20:4n-3	ND	ND	ND	(11.1%)0.3	ND	ND	ND	ND	ND	ND
C20:5n-3	ND	0.07	ND	ND	9.97	3.84	ND	ND	ND	ND
C22:4n-3	ND	ND	ND	(43.4%)0.23	ND	ND	ND	ND	ND	ND
C22:5n-6	ND	ND	ND	ND	ND	ND	0.64	0.55	ND	ND
C22:5n-3	ND	ND	ND	ND	ND	(24.0%)1.21	8.79	3.57	ND	ND
C24:0	0.65	0.43	1.41	0.58	1.38	0.78	1.45	1.35	0.89	0.67
C24:5n-3	ND	ND	ND	ND	ND	(73.6%)3.38	ND	(46.4%)3.09	ND	ND
Total Lipid	362	384	173	393	124	280	137	151	190	200

\*% conversion = product/(substrate + product)

ND= not detected

## Figure 58

1	ATGGAACATT	TCGATGCGTC	ACTCAGTACC	TATTTCAAGG	CCTTCCTGGG
51	CCCCCGAGAT	ACAAGAGTCA	AAGGATGGTT	CCTCCTGGAC	AATTACATCC
101	CTACGTTTGT	CTGTTCTGTT	ATTTACTTAC	TCATTGTATG	GCTGGGACCA
151	AAATACATGA	AGAACCGGCA	GCCGTTCTCT	TGCCGAGGCA	TCCTGCAGTT
201	GTATAACCTT	GGACTCACCC	TGCTGTCTCT	CTACATGTTT	TATGAGTTGG
251	TGACAGGTGT	GTGGGAGGGC	AAATACAAC	TTTTCTGCCA	GGGAACACGC
301	AGCGCGGGAG	AATCCGATAT	GAAGATCATC	CGCGTCCTCT	GGTGGTACTA
351	CTTCTCCAAA	CTCATCGAAT	TCATGGACAC	CTTTTTCTTC	ATCCTTCGCA
401	AGAACAACCA	CCAGATCACC	GTGCTCCATG	TCTACCACCA	CGCTACCATG
451	CTCAACATCT	GGTGGTTTGT	GATGAACTGG	GTTCCCTGCG	GCCATTCATA
501	TTTTGGTGCG	ACACTCAACA	GCTTCATCCA	TGTCCTCATG	TACTCGTACT
551	ATGGTCTGTC	CTCCATCCCG	TCCATGCGTC	CCTACCTCTG	GTGGAAAAAG
601	TACATCACTC	AAGGGCAGCT	GGTCCAGTTT	GTGCTGACAA	TCATCCAGAC
651	GACCTGCGGG	GTCTTCTGGC	CATGCTCCTT	CCCTCTCGGG	TGGCTGTTCT
701	TCCAGATTGG	ATACATGATT	TCCCTGATTG	CTCTCTTCAC	AAACTTCTAC
751	ATTCAGACTT	ACAACAAGAA	AGGGGCCTCT	CGGAGGAAAG	ACCACCTGAA
801	GGGCCACCAG	AACGGGTCTG	TGGCCGCCGT	CAACGGACAC	ACCAACAGCT
851	TCCCTTCCCT	GGAAAACAGC	GTGAAGCCCA	GGAAGCAGCG	AAAGGATTGA

## Figure 59

1 MEHFDASLST YFKAFLGPRD TRVKGWFLLD NYIPTFVCSV IYLLIVWLGP  
51 KYMKNRQPFS CRGILQLYNL GLTLLSLYMF YELVTGVWEG KYNFFCQGTR  
101 SAGESDMKII RVLWWYYFSK LIEFMDTFFF ILRKNNHQIT VLHVVYHHATM  
151 LNIWWFVMNW VPCGHSYFGA TLNSFIHVLM YSYYGLSSIP SMRPYLWWKK  
201 YITQGQLVQF VLTIIQTTCG VFWPCSFPLG WLFFQIGYMI SLIALFTNFI  
251 IQTYNKKGAS RRKDHLKGHQ NGSVAAVNGH TNSFPSELS VKPRKQRKD\*

Figure 60

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	PYX242	PRAE-87	PYX242	PRAE-87	PYX242	PRAE-87	PYX242	PRAE-87	PYX242	PRAE-87	PYX242	PRAE-87	PYX242	PRAE-87	PYX242	PRAE-87	PRAE-87
Substrate	GLA	GLA	AA	AA	ADA	ADA	STA	STA	STA	EPA	EPA	DPA	DPA	DPA	DPA	DPA	DPA
Concentration	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM
% total lipid																	
C18:1n-9	15.94	12.05	12.30	12.61	11.77	10.91	14.81	15.52	15.91	16.66	15.04	8.07					
C18:1n-7	1.25	8.00	1.10	9.60	1.13	8.87	1.19	8.94	1.33	11.60	1.37	6.90					
C18:3n-6	4.53	1.11	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C18:4n-3	ND	ND	ND	0.00	ND	0.14	2.78	0.80	ND	ND	ND	ND	ND	ND	ND	ND	ND
C20:1n-7	ND	0.98	ND	0.91	ND	0.63	ND	0.62	ND	0.94	ND	1.34					
C20:3n-6	0.10 (78.7%)	1	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C20:4n-6	ND	ND	11.44	11.28	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C20:4n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C20:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C22:4n-6	ND	ND	ND	(36.0%)	20.41	21.15	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C22:4n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C22:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C24:4n-6	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
C24:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Total Lipid	208	102	115	177	158	117	124	200	221	199	127	91					

(% conversion) = product/(substrate + product)  
 ND = not detected

## Figure 61

Host (plasmid)	334(pYXX242)	334(pRET-22)	334(pYXX242)	334(pRET-22)	334(pYXX242)	334(pRET-22)
Added Substrates	50 mM GLA	50 mM GLA	50 mM AA	50 mM AA	no substrate	no substrate
Fatty Acid		%total	lipid			
C16:0	19.8	18.59	13.8	6.23	13.62	13.63
C16:1n-7	20.92	17.74	26.62	13.01	40.1	47.67
C18:0	5.79	4.94	3.62	2	4.86	5.031
C18:1n-7	(3.9%) 0.85	(9.12%) 1.78	(3.5%) 0.97	(12.54%) 1.18	(3.6%) 1.5	(7.53%) 3.88
C18:1n-9	8.46	7.45	10.27	5.36	13.7	16.93
C18:3n-6	*26.62	*22.03	0.03	0.01		
C20:3n-6	(1.1%) 0.3	(38.2%) 13.61				
C20:4n-6			*27.36	*65.38		
C22:4n-6						
Total lipid (μg)	36	42	85	280	55	79
(% conversion)=product/(substrate+product)						
* indicates substrate added						



Figure 62

A.

Host(plasmid)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)
Added substrate	50 $\mu$ M SA C18:0	50 $\mu$ M OA C18:1n-9	50 $\mu$ M LA C18:2n-6	50 $\mu$ M DGLA C20:3n-6	25 $\mu$ M AA C20:4n-6	50 $\mu$ M Adrenic C22:4n-6	
Fatty Acid	% total lipid						
C16:0	12.9	12.54	15.23	9.1	10.2	3.42	
C16:1	37.71	23.83	24.87	16.61	18.375	7.66	
C18:0	11.44	4.7	4.49	2.7	2.9	1.23	
C18:1n-9	14.03	*16.87	9.54	6.74	6.39	2.99	
C18:2n-6			16.87		0.15	0.28	
C18:3n-6							
C20:2n-6						0.05	
C20:3n-6							
C20:4n-6							
C22:4n-6							
Total Lipid ( $\mu$ g)	63	103	71	110	97	277	

\*44.34  
0.34  
\*25.78  
\*75.72

B.

Host(plasmid)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)
Added substrate	50 $\mu$ M ALA C18:3n-3	50 $\mu$ M PA C18:0	50 $\mu$ M EPA C20:5n-3	50 $\mu$ M STA C18:4n-3
Fatty Acid	% total lipid			
C16:0	13.91	15.06	16.92	20.08
C16:1	14.74	31.77	23.57	20.17
C18:0	4.06	*4.85	4.94	6.02
C18:1n-9	6.65	13.59	10.46	9.29
C18:3n-3	*38.66			
C18:4n-3				*20.45
C20:4n-3				(12.57%) 2.94
C22:5n-3			*15.48	
Total Lipid ( $\mu$ g)	80	84	81	60

\* indicates substrate added  
(% conversion) = product/(substrate+product)

Figure 63

A.

Host(plasmid)	334(pRET-22+pCGR-4)	334(pYX242+pYES2)
Addc substrate	50μM GLA	50μM GLA
Fatty Acid	% total lipid	
C16:0	15.92	15.07
C16:1n-7	24.97	19.48
C18:0	8.52	6.48
C18:1n-7	3.9	1.61
C18:1n-9	18.48	12.71
C18:3n-6	*7.0	*10.54
C20:0	0	0
C20:3n-6	(27.81%) 4.36	(1.58%) 0.17
C20:4n-6	(27.55%) 4.32	0
Total Lipid (μg)	508	168

B.

Host(plasmid)	334(pRET-22+pCGR-4)	334(pYX242+pYES2)
Addc substrate	50μM STA	50μM STA
Fatty Acid	% total lipid	
C16:0	18.74	16.21
C16:1n-7	21.35	26.09
C18:0	6.78	7.57
C18:1n-7	1.97	1.7
C18:1n-9	20.73	22.41
C18:4n-3	*6.05	*13.43
C20:0	0	0.45
C20:4n-3	(15.88%) 1.68	(4.73%) 0.69
C20:5n-3	(26.93%) 2.85	(3.22%) 0.47
Total Lipid (μg)	335	161

\* indicates substrate added  
 (% conversion) = product/(substrate+product)